STIC-Biotech/ChemLib

From: S nt: To: Subject:

Ford, Vanessa Thursday, October 11, 2001 1:28 PM STIC-Biotech/ChemLib In re: 09596101 Sequence Search

Please search SEQ ID NO: 1. Please search SEQ ID NO. 3. Please include an interference search.

Vanessa L. Ford **Biotechnology Patent Examiner** Office: CM1 8D17

Mailbox: CM1 8E12 ► Phone: 703.308.4735 Apturit Please

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SEARCH REQUEST FORM

50795

Scientific and Technical Information Center

Requester's Full Name:		Examiner # +	Date:
An Olini Phone	Number 30	Samul Niverban	·
Mail Box and Bldg/Room Location	on:	Results Format Preferred to	circle): PAPER DISK E-MAIL
If more than one search is subr	mitted, please pri	oritize searches in order	of need.
Please provide a detailed statement of the Include the elected species or structures, utility of the invention. Define any term known. Please attach a copy of the cover	e search topic, and des keywords, synonyms, s that may have a spec	cribe as specifically as possible to acronyms, and registry numbers.	he subject matter to be searched.
Title of Invention:			
Inventors (please provide full names):			
Earliest Priority Filing Date:	·		,
For Sequence Searches Only Please inclu appropriate serial number.			sued patent numbers) along with the

STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher: (Wessen - Willy	NA Sequence (#)	
Searcher Phone = 308-458/	AA Sequence (#) 2	Dialog
Searcher Location. Blotech lub.	Structure (#)	Questel:Orbit
Date Searcher Picked Up. 10/11/0/	Bibliographic	Dr Link
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Searcher Prep & Review Time	Fulltext	Sequence Systems ABSSOZ
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OM protein - protein search, using sw model
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Listing first 45 summaries
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SUMMARIES

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AAG44125	AAY32318	AAR88406	AAR11599	AAW29456	AAW29457	AAW29455	AAB52463	AAR97362	AAY24914	AAY24915	ID
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ALIGNMENTS

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Claim 1; Page 45; 49pp; English.	foetida polypeptides derived from coelomic cytolytic factor 1	WPI; 1999-385905/32.	De Baetselier P;	THE BUY THE PROPERTY AND THE PLOTECTION.	CORPORED AND THE STATE STATE TAGE TO STATE TO ST	1997; 9/67-02039/4.	1998; 98WO-EP08169.		1	 29-A2.	floetida	inflammation; immunology.	sdmal infection; bacterial infection; tumour therapy;	foetida; coelomic cytolytic factor 1; CCF-1; cancer;	Eisenia foetida coelomic cytolytic factor l peptide.	1990 (first entry)	5	AAY24915 standard; peptide; 13 AA.		•	

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RESULT
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         The present sequence represents a Eisenia foetida coelomic cytolytic CC factor 1 (CCF-1) peptide. The CCF-1 protein has antiparasitic, CC antibacterial and antiinflammatory activity. Recombinant coelomic CC cytolytic factor 1 (CCF-1) is trypanolytic for the African trypanosome CC cytolytic factor 1 (TCCF-1) is trypanolytic for the African trypanosome CC Trypanosoma brucei in a dose-dependent manner. The trypanolytic activity CC of rCCF-1 can be inhibited by anti-CCF-1 and anti-tumour necrosis factor CC (TMF)/TIP monoclonal antibodies. Furthermore, N,N'-diacetlychitobiose CC corroborate the findings that CCF-1 shares a trypanolytic, lectin-like CC corroborate the findings that CCF-1 shares a trypanolytic, lectin-like CC corroborate the findings that CCF-1 shares a trypanosomal or CC domain with TMF-alpha. CCF-1 is useful to treat trypanosomal or CC cuseful in tumour therapy, inflammation and other areas of immunology. CT constituted is derived from a 42 kDa cytolytic protein named CC CCF-1 that binds lipopolysaccharide and beta-1,3-glucan. The factor cresembles the vertebrate tumour necrosis factor-alpha (TMF-alpha), and CC may be used as an alternative for TMF-alpha.
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The present sequence represents the Eisenia foetida coelomic cytolytic factor 1 (CCF-1). The protein has antiparasitic, antibacterial and antiinflammatory activity. Recombinant coelomic cytolytic factor 1
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DB; AAX83611.
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                                                                                                                                           Savva
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                                              DNA construct encoding enzyme with beta-1,3-glucanase activity useful for modifying or degrading beta-glucan contg. material \epsilon the prepn. of e.g. food colourants, flavourings and yeast extra
                        Claim 1;
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N-PSDB; AAT29043.
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                                                  yeast extracts
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                                                                and in
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A novel

beta-1,3-glucanase (AAR97362) from Oerskovia xanthineolytica

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RESULT
AAB52463
                                                       Query Match
Best Local
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Best Local (
                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLG109 is useful for degrading or modifying beta-glucan-contg. material. Its amino acid sequence was deduced from a genomic DNA sequence (AAT29043) isolated from an O. xanthineolytica library. Recombinant beta-1,3-glucanase can be produced on a large scale using transformed host cells, esp. Bacillus subtilis DN1885 or Toc46. Protease-free beta-1,3-glucanase can be obtd. that is useful for lysing fungal cell walls, allowing recovery of intracellular proteins. The enzyme is also useful for the prepn. of protoplasts and for the bred.
                                                                                                                                                                                           The present invention relates to Mycobacterium tuberculosis secreted proteins (MTSP), where the polypeptide has M. tuberculosis specific antigenic and immunogenic properties. Compositions of the invention may be useful for diagnosing Mycobacterium tuberculosis infection and as a
                                                                                                                                                                                                                                                                                                                                      Novel Mycobacterium tuberculosis secreted polypeptides and polynucleotides useful in diagnosis, treatment and prophyltuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAY-1999;
04-MAY-1999;
                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                           Claim 11; Fig 1; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-007151/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB52463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB52463 standard; protein; 294 AA
                                                                                                                                                                           vaccine against M.
                                                                                                                                                                                                                                                                                                                                    tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PUBL-) PUBLIC HEALTH RES INST NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200066143-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for the prodn. of pigments, colorants, flavours, yeast extract
SGEIDIIETIGN 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sgeidimenvgn 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
9; Conserv
                                  Similarity
9; Conserv
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                                                                                                                                    294
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                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gomez MJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tuberculosis secreted protein; MTSP; vaccine
                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0132479.
99US-0132503.
                                                                                                                                                                           tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.1%;
75.0%;
                                                       70.3%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    secreted protein #28
                                    1;
                                                     Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 50; I
Pred. No. 0.
                                  Mismatches
                                                                                                                                                                         infection
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                                                                           DB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .12;
                                                                           22;
                                    2;
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                                                                           Length 294;
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Best Local Matches

Similarity 8; Conser

Conservative

Indels

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Gaps

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RESULT
AAW29455
ID AAW2
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             Query Match
Best Local (
                                                                                                                                        This polypeptide comprises a novel Oerskovia xanthineolytica (OX) enzyme that exhibits beta-1,3-glucanase (Bg) activity. Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT89155). Claimed DNA constructs that encode the novel BG (see also AAW29456 for corrected sequence), a mannose binding domain (see AAW29459) or a full-length enzyme, i.e. BG with mannose binding domain (see AAW29456), can be used to produce recombinant BG polypeptides, with or without a mannose binding domain, in fungal or bacterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, especially for the gentle lysis of microbial cell walls, thereby enabling recovery of desirable intracellular products with a reduced amount of contaminants. They can also be used for the
                                                                                                                                                                                                                                                                                                                                                                   New isolated beta-1,3-glucanase enzyme xanthineolytica, used particularly for
                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-526451/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diers I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AUG-1996;
12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oerskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beta-1,3-glucanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW29455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW29455 standard, Protein;
                                                                 Sequence
                                                                                           studies.
                                                                                                      production of e.g. pigments, colourants, flavourants, yeast extracts, pharmaceuticals, food or feed compositions, and to prepare protoplasts for use in fusion, transformation and co
                                                                                                                                                                                                                                                                                                                                 Example
                                                                                                                                                                                                                                                                                                                                                        for obtaining desirable products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NOVO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9739114-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fungal cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oerskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sgeidliewygn
                                                                                                                                                                                                                                                                                                                                2; Page 35-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOVO-NORDISK
                                                                                                                                                                                                                                                                                                                                                                                                               AAT89155
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferrer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xanthineolytica mature beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xanthineolytica LLG109
                                                                 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96DK-0000885
96DK-0000427
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23..120
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164..952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e; lytic enzyme; yeast; beta glucan degradation;
intracellular product; purification; protoplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
             68.8%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halkier
                                                                                                                                                                                                                                                                                                                                64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
Score 44; DB Pred. No. 1.4; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hedegaard L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DSM 10297).
                                                                                                                                                                                                                                                                                                                                                                       the
          DB
                                                                                                                                                                                                                                                                                                                                                                      obtained from Oerskovia
he lysis of microbial cells
                           18;
                        Length 263;
                                                                                                      and cloning
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SGEIDIIETIG 11

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RESULT
AAW29457
                                                                           38888888888888888888888888
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Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Peptide
                                                                                                                                                polypeptides, with or without a mannose binding domain, in fungation or bacterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, especially for the gentle lysis of microbial cell walls, thereby enabling recovery of desirable intracellular products with a reduced amount of contaminants. They can also be used for the production of e.g. pigments, colourants, flavourants, yeast
                                                                                                                                                                                                                                                          This sequence comprises the polypeptide precursor of a novel oerskovia xanthineolytica enzyme that exhibits beta-1,3-glucanase (BG) activity. Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT89157). Claimed DNA constructs that encode the novel BG (see also AAW29455), a mannose binding domain (see AAW29458) or a full-length enzyme, i.e. BG with mannose binding domain (see AAW29456), can be used to produce recombinant BG binding domain (see AAW29456), can be used to produce recombinant BG
                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 42-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated beta-1,3-glucanase enzyme - obtained from Oerskovia xanthineolytica, used particularly for the lysis of microbial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-526451/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diers I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-AUG-1996;
12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09739114-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oerskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beta-1,3-glucanase; lytic enzyme; yeast; beta glucan degradation;
fungal cell wall; intracellular product; purification; protoplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oerskovia xanthineolytica beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW29457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW29457 standard; Protein; 303
                                                                                                                      prepare protoplasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                obtaining desirable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sgeidimenvg 126
                                                                                                                                      n of e.g. pigments, colourants, flavourants,
pharmaceuticals, food or feed compositions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         xanthineolytica LLG109 (DSM 10297).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ferrer P,
                                                                           303
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96DK-0000885.
96DK-0000427.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Sig_peptide 53..303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                      for use in fusion,
            68.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                       64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     products
Score 44; DB Pred. No. 1.7; 2; Mismatches
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hedegaard L;
                                                                                                                      transformation and cloning
                              DB 18;
                           Length 303;
 Indels
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                                                                                                                                                                                                                                              in fungal
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Gaps
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RESULT
AAW29456
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sequence
novel BG
                                                                              novel BG lacking a MBD (see AAW29455 and AAW29457), a MDB (see AAW29458), or the full-length enzyme can be used to produce recombinant BC polypeptides, with or without a mannose binding domain, in fungal or bacterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, especially for the gentle lysis of microbial cell walls, thereby enabling recovery of desirable intracellular products with a reduced amount of contaminants. They can also be used for the
                                                                                                                                                                                              This sequence comprises the polypeptide precursor of a novel oberskovia kanthineolytica enzyme that exhibits beta-1,3-glucanase (BG) activity and which includes a mannose binding domain (MBD). Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT89156). Claimed DNA constructs that encode the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                        production of e.g. pigments, colourants, flavourants,
extracts, pharmaceuticals, food or feed compositions,
                                                                                                                                                                                                                                                                                                                New isolated beta-1,3-glucanase enzyme - obtained from Oerskovia xanthineolytica, used particularly for the lysis of microbial cells for obtaining desirable products
                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-526451/48.
N-PSDB; AAT89156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beta-1,3-glucanase; lytic enzyme; yeast; beta glucan degradation; fungal cell wall; intracellular product; purification; protoplast.
                            prepare protoplasts studies.
                                                                                                                                                                                                                                                                                                                                                                                                                     Diers I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-AUG-1996;
12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oerskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oerskovia xanthineolytica beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-APR-1998
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Sequence
                                                                                                                                                                                                                                                                                     Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9739114-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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||||||:|:|
9 sgeidimenvg 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein; 435 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   Ferrer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     xanthineolytica LLG109 (DSM 10297).
 435
                                                                                                                                                                                                                                                                                     Page 39-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96DK-0000885.
96DK-0000427.
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53..435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Mannose-binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Mat_protein
                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                   Halkier T,
                                                                                                                                                                                                                                                                                    64pp; English.
                                           use
                                           in fusion,
                                                                                                                                                                                                                                                                                                                                                                                                                   Hedegaard
                                           transformation and cloning
                                                                                                                                                                                                                                                                                                                                                                                                                   ŗ
                                                                       yeast
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Query Match Best Local :

Similarity

68.8%;

Score 44; DB Pred. No. 2.5;

18;

Length 435;

RESULT
AAR11599
ID AAR1
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AC AAR1
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Matches

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est Local Similarity
atches 7; Conserv
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                                               Yeast; fungus; enzyme; endo-beta-glucanase; EC-3.2.1.6; hydrolase; endo-1,3(4)-beta-glucanase; beta-glucan degradation; hydrolysis; detergent; surfactant; fungicide; antifungal; cleaning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat resistant beta-1,3-glucanase gene DNA - alkali-compatible Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1991-113290/16.
N-PSDB; AAQ11293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-1991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta-1,3-glucanase
W09531533-A1
                                                                                                    Trichoderma harzianum endo-1,3(4)-beta-glucanase
                                                                                                                              19-AUG-1996
                                                                                                                                                       AAR88406
                                                                                                                                                                                 AAR88406 standard; Protein; 292 AA.
                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Fig 2; llpp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SHKJ ) SHINGIJUTSU KAIHATSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alkalophilic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUN-1991
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                        Trichoderma harzianum CBS
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119 geidimervnn 129
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9 sgeidimenvg 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heat resistant
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AAY32318
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foods and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              raised against a pure endo-1,3(4)-beta-glucanase from T. harzianum CBS 243.71. Using this sequence, the protein may be expressed recombinately in transformed host cells, particularly Aspergillus oryzae of Aspergillus niger. Typical applications of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This polypeptide is immunologically reactive with antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding endo-beta-glucanase from Trichoderma harzianum useful, e.g., in food processing, as antifungal agent, in cleaning compsns., etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-010920/01.
N-PSDB; AAT09876.
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Kauppinen MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-NOV-1995.
                                                                                                                                                                                               WO9955887-A2
                                                                                                                                                                                                                                               Beta-carotene hydroxylase; corn; maize;
carotenoid; zeaxanthin; pigment.
                                                                                                                                                                                                                                                                                     Corn beta-carotene hydroxylase.
                                                                                                                                                                                                                                                                                                               28-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                 AAY32318 standard; Protein; 223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinantly produced protein are preparation of protoplasts and yeast extracts, brewing, wine and press juice manufacture, foods and feeds, as antifungal agents, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 40; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAY-1994;
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Novel carotenoid biosynthesis enzyme polynucleotides and polypeptides
                       WPI; 2000-062037/05
N-PSDB; AAZ34967.
                                                               Cahoon RE,
                                                                                                                 24-APR-1998;
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                                                                                        (DUPO ) DU PONT DE NEMOURS & CO
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158 geidimetv 166
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                                                              Kinney AJ,
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77.8%;
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AAG44125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the deduced amino acid sequence of the C-terminal three Quarters of a corn beta-carotene hydroxylase derived from isolated CDNA clones (see AAZ34967). The enzyme converts beta-carotene into Zeaxanthin. The invention provides movel carotenoid biosynthesis C enzymes, specifically beta-carotene hydroxylase, lycopene cyclase C and lycopene epsilon cyclase (see AAZ3496774). The enzymes may be polynucleotides encoding them (see AAZ34967774). The enzymes may be create transgenic plants in which the enzymes may be cyclase to create transgenic plants in which the enzymes or compared recombinantly and used to raise antibodies, used for cyclase to create transgenic plants in which the enzymes are cyclase or cyclase to create transgenic plants in which the enzymes or cyclase they are not normally found. This cyclase cyclase activity products, and so is a desirable poultry feed additive. Blocking of beta-carotene of bydroxylase activity may create a high beta-carotene corn which may be valuable for human consumption. The enzymes can also be used as targets to facilitate the design of the enzymes can also be used as targets to facilitate the design of the enzymes could lead to an inhibition of plant growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 59. Best Local Similarity 60. Matches 6; Conservative
 25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
29-MAR-1999
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08-APR-1999
16-APR-1999
11-APR-1999
21-APR-1999
23-APR-1999
                                                                                                                                                                     25-FEB-2000;
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                                                                                                                                                                                                                                        Arabidopsis thaliana.
                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID
                                                                                                                                                                                                                                                                                                                                                             AAG44125;
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24 gevpvietlg 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 AA;
                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                     2000EP-0301439
990S-0121825
990S-0123180
990S-0125788
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                                                                                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                                                                                  termination sequence
                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                 Arabidops'is thaliana protein fragment
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75 evdv¦qvign 84
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5; Conservative
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990S-0121825

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990S-0128714

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50.0%;
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990S-0140991 990S-0141287 990S-0141287 990S-0142154 990S-0142390 990S-0142920 990S-0142927 990S-0144085 990S-0144085 990S-0144085 990S-0144331 990S-0144331 990S-0144332 990S-0144331 990S-0144331 990S-0144331 990S-0144331 990S-0144331 990S-0144331 990S-0144335 990S-0144335 990S-0144335 990S-0144335 990S-0144335 990S-0144335 990S-0144335 990S-0144335	990S-0132487 990S-0134218 990S-0134219 990S-0134221 990S-0134768 990S-0135124 990S-0135629 990S-0136782 990S-0137522 990S-0137522 990S-0137522 990S-0137522 990S-0137522 990S-0137522 990S-0139454 990S-0139454 990S-0139454 990S-0139454 990S-0139456 990S-0139456 990S-0139456 990S-0139453
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RESULT 13
AAG44123
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  25-FEB 1999
05-MAR 1999
09-MAR 1999
23-MAR 1999
25-MAR 1999
25-MAR 1999
06-APR 1999
06-APR 1999
16-APR 1999
16-APR 1999
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31-MAY 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
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124 evdvlqvign 133
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990S-0160989
990S-0161404
990S-0161406
990S-0161406
990S-0161359
990S-0161350
990S-0161361
990S-0161920
990S-0161920
990S-0161920
990S-0161923
 990S-0121825

990S-012548

990S-0125788

990S-0126785

990S-0127462

990S-0128234

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990S-0128234

990S-0130077

990S-013049

990S-0130510

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990S-013048

990S-013149

990S-013248

990S-013248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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50.0%;
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22-MAY 1999
23-MAY 1999
24-MAY 1999
25-MAY 1999
26-MAY 1999
27-MAY 1999
27-MAY
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9908-0137502

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9908-0139454

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9908-0139460

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9908-0139461

9908-0139463

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9908-013963

9908-0140823

9908-0140823

9908-0141842

9908-0141842

9908-014255

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99US-0135124.
99US-0135353.
99US-0135629.
99US-0136392.
99US-0136392.
99US-0136782.
            99US-0144086.
99US-0144331.
99US-0144332.
99US-0144334.
99US-0144334.
99US-0144884.
99US-0144884.
99US-0145086.
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99US-0145087.
  9905-0145918
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11-AUG-12-AUG-13-AUG-13-AUG-16-AUG-17-AUG-

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RESULT 14
AAE00115
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Best Local S
Matches 5
                                               corresponding nucleic acid sequences and variants. RP-II protease is useful as a constituent in additives, detergent compositions and other cleaning compositions, optionally in combination with other enzymes such as proteases, lipases, cellulases, maylases, peroxidases or oxidases. The variants of RP-II have improved properties such as substrate specificities, catalytic rate, stability, especially towards the action of proteolytic enzymes and improved resistance towards peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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Synthetic:
peroxidase. Note: This sequence is not shown in the specification but is derifund the mature B. licheniformis RPII protein [SEQ ID NO: 2] show page 101-102 of the specification (AAE00011). The specification a refers to following variants: (a) VIF, (b) D7G+T125S+E152G+N182I,
                                                                                                                                                                                                                                                                  Norregaard-madsen J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Residual proteas mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE00115
                                                                                                                                                    The present sequence is Bacillus licheniformis variant (T109R).
                                                                                                                                                                                       Example
                                                                                                                                                                                                           Novel RP-II type protease and its variants useful as constituents detergent; compositions, additives and cleaning compositions - \,
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20-OCT-1999;
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protease II; RP-II;
mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               licheniformis RP-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; Protein; 222
                                                                                                                                                                                      Page -; 132pp;
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990S-0161360.
990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
990S-0162142.
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99DK-0001500
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                                                                                                                                                                                                                                                                                Rahbek Ostergaard
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Wild type Thr substituted with Arg"
                                                                                                                                                                                       English.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         additive; cleaning composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protease
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              variant (T109R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                              Voge Christensen
                                                                                                                                                                (BLC) RP-II protease
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                          : is derived
2] shown in
              shown in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detergent;
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RESULT 15
AAB70788
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                                          This invention describes a novel isolated nucleic acid (I) from the genome of phage phi-CH1 of Natrialba magadii. The genome of phi-CH1 is a combination of 48300 and 10198 base pair sequences (S1 and S2), both combination of 48300 and 10198 base pair sequences (S1 and S2), both combination of 48300 and 10198 base pair sequences (S1 and S2), both combinant vector (RVI) containing at least one copy of (I); convel (I) recombinant vector (RVI) containing the ori of phi-CH1; (3) cell transformed with RVI or RV2; (4) isolated polypeptide (II) encoded by (I); N. magadii cells free from the prophage of phi-CH1; (5) phage variants having lytic properties different from those of wild-type phi-CH1 and having genomic sequences at least 70 % homologous with the phi-CH1 genome; (6) use of phi-CH1 as gene transfer vector; and (7) use of halophilic Archaea for production of proteins and other polymers. Specifically N. magadii, for production of proteins and other polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome; halophilic; polyhydroxybutyrate; inducible expression; 6\text{-methyltrans} ferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N. magadaii bacteriophage phi-CHl 6-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB70788;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 41-42; 72pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid from phage phichl, expressing proteins and polymers in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Witte A, Baranyi U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-AUG-1999;
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Natrialba magadii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAF61284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-245930/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LUBI/) LUBITZ W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-FEB-2001
     inducible
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98 gaielsepignr 109
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                         poly(hydroxybutyrate)). Vectors containing
expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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58.3%;
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Pred. No. 39;
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Query Match
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Matches 6
3 EIDIIETIGNR 13
                 Similarity 6; Conserv
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                        56.2%;
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                       Score 36;
Pred. No.
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Search completed: October 11, 2001, 15:51:38 Job time: 201 sec

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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
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US-09-137-440-44

US-09-330-945-2

US-09-396-651B-2
5180808-2

US-07-621-193A-5

US-08-018-489C-5

US-08-008-962-1

US-08-675-507-1

US-09-213-205-1

US-07-906-395-2

US-08-192-632-2

US-08-190-676-2

US-08-190-676-2

US-09-099-902B-2

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13.985 Million cell updates/sec
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US-08-824-707-2; Sequence 2, Ap; Patent No. 591

Application US/08824707

APPLICANT:

Ferrer, Diers, :

, Pau Ivan

INFORMATION:

32 50.0 1/4 1 US-08-34-34-34-3-3 32 50.0 114 1 US-08-33-305-6 32 50.0 114 1 US-08-726-817-6 32 50.0 114 1 US-08-726-817-6 32 50.0 114 2 US-08-725-969-6 32 50.0 114 2 US-08-794-524-6 32 50.0 114 2 US-08-794-524-6 32 50.0 114 2 US-08-994-0393-6 32 50.0 114 5 PCT-US94-03793-3 32 50.0 162 1 US-08-300-903A-3 32 50.0 162 1 US-08-303-305-5 32 50.0 162 1 US-08-284-393B-9 32 50.0 162 1 US-08-284-393B-9 32 50.0 162 1 US-08-726-817-5 32 50.0 162 1 US-08-726-817-5 32 50.0 162 2 US-08-726-817-5 32 50.0 162 2 US-08-726-817-5 32 50.0 162 2 US-08-726-817-5 32 50.0 162 2 US-08-794-524-5 32 50.0 162 2 US-08-794-524-5 32 50.0 162 2 US-08-794-524-5 32 50.0 162 2 US-08-794-524-5	45	44	43	42	41	40	39	38	37	36	35 5	34	ω ω	32	31	30	29	87
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1 US-08-93 1 US-08-93 1 US-08-72 1 US-08-72 1 US-08-72 1 US-08-72 2 US-08-72 2 US-08-72 1 US-08-30 1 US-08-39 1 US-08-39 1 US-08-72 1 US-08-72	50.0	50.0	50.0	50.0	50.0	50.0	•		•	•	•	•	•	•	٠	•	•	00.0
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	US-09-189-193-5	US-08-794-524-5	-08-725-969	-08-504-042	-08-726-817	:-08-284-393B-	US-08-393-305-5	US-08-031-399-2	US-08-300-903A-3	PCT-US94-03793-3	US-09-189-193-6	US-08-794-524-6	-08-725-969	-08-504-042	-08-726-817-	:-08-393-305-	-08-03	-08-343
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; TYPE: amino a
; TOPOLOGY: lir
; MOLECULE TYPE:
US-08-824-707-2
                  Query Match'
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,707
FILING:DATE: 14-April-1997
FILING:DATE: 14-April-1997
CLASSIFICATION: 4.35
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 4290.204-US
                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 306 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hedegaard, Lisbeth
APPLICANT: Halkler, Torben
APPLICANT: Asenjo, Juan
APPLICANT: Savva, Demitris
TITLE OF INVENTION: No. 5919688el enzyme with beta-1,3-glucanase activity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 59196880 No. 591968disk of No. 5919688th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
1 SGEIDIIETIGN 12
                                                                                                                                                                           amino acid
)GY: linear
                                      Conservative
                                                                                                                                                         protein
                                                        78.1%;
75.0%;
                                      ?
                                                      Score 50; DB 2
Pred. No. 0.09;
                                      Mismatches
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                                      Indels
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                                                                                                                                             RESULT
                                                                                       Sequence 4, Approx. 1966
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/CO
FILING DATE: 11-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bogosian, Elizabeth A.
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 63475/97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jack Goldstein, Alex Zhu and Lin
TITLE OF INVENTION: ENDO-BETA-GALACTOSIDASE
NUMBER OF SEQUENCES: 13
                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
   FITLE OF INVENTION:
                                APPLICANT:
                                                                APPLICANT:
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146 NGEIDIMEHVG 156
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                                                                                                                                                                                                                                                       Local Similarity les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
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                                                                             INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 amino acids
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              Andersen, Lene No. 58719
Kauppinen, Markus Sakari
Christgau, Stephan
                                                                                                                                                                                                                                                                                                                                                   gub, Rhodothermus marinus
                                                                                                                                                                                                                                                        Conservative
                                                                Kofod, Lene Venke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: 3.5 INCH 1.44 Mb STORAGE DISKETTE IBM PC COMPATIBLE SYSTEM: MS-DOS
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                                                                                                                                                                                                                                                                     63.6%;
An Enzyme With Endo-1,3(4)-B-Glucanase
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Best Local
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CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/737,526
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Valeta, Gregg A
REGISTRATION NUMBER: 35,127
REGISTRATION NUMBER: 35,127
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS: ADDRESSE: No. 61400960 No. 6140096d1sk of No. 6140096th America, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
PRIOR APPLICATION DATA:
                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                               APPLICANT: Kauppinen, Markus Sakari
APPLICANT: Christgau, Stephan
                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                    ADDRESSEE: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 GEIDIMETV 166
                                                                                       COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                       CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 292 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Dis
COMPUTER: IBM CO
OPERATING SYSTEM:
                               FILING DATE
                                          APPLICATION NUMBER:
                                                                           SOFTWARE:
                                                                                                                                                       COUNTRY: USA
ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09098580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: No. 5871966o No. 5871966disk of No. 5871966th America, Inc. 405 Lexington Avenue
                                                                                                                                                                                                                    405 Lexington Avenue
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                                                                                                                                                                                                                                                                                                                                                Andersen, Lene No.
                                                                                                                                                                                                                                                                                                                                                                 Kofod, Lene Venke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                           FastSEQ for Windows Version 2.0
                                                                                                        IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
                                                                                                                          Diskette
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                                                                                                                                                                                                                                                                                  An Enzyme With Endo-1,3(4)-B-Glucanase Activity
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77.8%;
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                                              US/09/098,580
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                                                                                                                                                                                                                                                                                                                                                  6140096boe
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: THM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,828C
FILING DATE: 28-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                  TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                 NAME: CAMPBELL, PAULA A REGISTRATION NUMBER: 32,503 REFERENCE/DOCKET NUMBER: FJI TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acid
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 GEIDIMETV 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT: MUTA, TATSUSHI
PPLICANT: SEKI, NORIAKI
PPLICANT: ODA, TOSHIO
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 28-FEE CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: BOSTON
STATE: MA
                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                   TOPOLOGY:
                                                                                 TYPE: amino acid
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & NDRESSEE: THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 STATE STREET
                                                                                                   262 amino acids
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                                                   linear
                                 peptide
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77.8%;
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Pred. No.
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                                                                      NAME/KEY: Protein LOCATION: 1..262 OTHER INFORMATION: US-09-330-945-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-330-945-37; Sequence 37; A
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Best Local Similarity
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            Query Match
Best Local S
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 Matches
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                                                                                                                                                                                                                                TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                             NAME: PITCHER, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: FJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ
ADDRESSEE: THIBEAULT, LLP
                                                                                                                                 MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB
TITLE OF INVENTION: AMEBOCYTE LYSATE FACTOR G SUBUNIT
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 SGEIDVMEARG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: BOSTON
STATE: MA
                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                     ENGTH:
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Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 HIGH STREET
                                                                                                                                                                                                      262 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUTA, TATSUSHI
SEKI, NORIAKI
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 Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                               peptide
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                57.8%;
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                                                                                     /note= "BG1 A1 SEQUENCE (FIGURE 2)"
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Pred. No.
             Score 37; DB
Pred. No. 19;
   Mismatches
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                            Length 262;
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   Indels
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130 SGEIDVMEARG

US-08-712-072C-3

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Query Match
Best Local Similarity
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                                                                                                                                                  US-08-476-008-44
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                                                                                                                                  Sequence 44,
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                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 286-0854 or 286-0082 TELEX: TWX 710-581-4766 INFORMATION FOR SEQ ID NO: 3:
                                                                                                   GENERAL
                                                                                                                                                                                                                                                                                                                                                                      08-712-072C-3
                                                APPLICANT: APPLICANT: APPLICANT:
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MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/01
FILING DATE: 11-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPA:
OPERATING SYSTEM: MS-DC
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jack Goldstein, Alex Zhu and Lin
TITLE OF INVENTION: ENDO-BETA-GALACTOSIDASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: PO
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 634
FELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-595
TELEPHONE: (212) 697-595
                                                                                                                                                                                                                   |||||::| |
189 SGEIDVMEARG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 321 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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STATE: NY
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STREET: 9
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                                                                                                                                                                                                                                                  1 SCEIDIIETIG 11
                                                                                                  INFORMATION:
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                                                                                                                     5627061
                                                                                                                                  Application US/08476008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SD
                             Kishore, Ganesh M.
Padgette, Stephen R.
Stallings, William C.
                                                                                    Barry, Gerard F.
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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63.6%;
5-Enolpyruvylshikimate-3-Phosphate Synthases
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Pred. No.
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                                                                                                                                                                                                                                                                                 Indels
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US-08-306-063-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match .
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                        Patent No. 5633435
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acid
                                                                                                                                                         APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, Willliam C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 0
FILING DATE: 13-SEP-1994
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (314)537-6099
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                          CORRESPONDENCE ADDRESS:
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NAME: Hoerner Jr., Dennis R.
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                                                                                                                                                                                                                                                                                                                                                                                                                     265 SGIIDIVEKMG 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/476,008 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: PatentI
                                                                    STATE: Missouri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                     COUNTRY: UZIP: 63198
                                                                                     CITY: St. Louis
                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                              Application US/08306063
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                                                                                                        E: Dennis R. Hoerner, Jr., Monsa
700 Chesterfield Village Parkway
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700 Chesterfield Village Parkway
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SYSTEM: PC-DOS/MS-DOS
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28-AUG-1991
Floppy disk
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Pred. No.
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                                                                                                                         Monsanto Co. BB4F
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44,
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                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,485
FILING DATE: 07-APR-1997
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NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
       PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: US 08/306,063
                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
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PRIOR APPLICATION NUMBER: US 07/749,611
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                CITY: St. Louis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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APPLICATION NUMBER: US 0 FILING DATE: 13-SEP-1994
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Padgette, Stephen R.
Stallings, William C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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63.6%;
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Pred. No. 80;
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8 No. 6248876
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Best Local
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INFORMATION FOR SEQ ID NO:
             FILING DATE: 28-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
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                                                                                              APPLICATION NUMBER: US 0
FILING DATE: 13-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                         STREET: 700 cue.
CITY: St. Louis
                                                                                                                                  APPLICATION NUMBER: US 08/833,485 FILING DATE: 07-APR-1997
                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 38-:
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                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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700 Chesterfield Village Parkway
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VENTION: Glyphosate Tolerant
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UMBER: US 07/576,537
31-AUG-1990
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                                                                                                                  us 08/306,063
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Monsanto Co. BB4E
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Query Match
Best Local Similarity
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                                              Query Match
Best Local Similarity
                               Matches
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                                                                                                                                                                       TELEFAX: (617) 248-7100
NFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 654 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
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                                                                                                                           TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: CAMPELL, PAULA A
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-033
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 28-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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1 SCEIDIIE 8
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53 STATE STREET
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SEKI, NORIAKI
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Pred. No.
                                              Score 34; DB 1;
Pred. No. 2e+02;
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Best Local Similarity

Matches 7; Conserv
                                                                                                                             Sequence 2, Application US/09396651B Patent No. 6225076
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                                             APPLICANT: 'Darst, Seth A
APPLICANT: Zhang, Gongyi
APPLICANT: Campbell, Elizabeth
APPLICANT: Minakin, Leonid
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                               APPLICANT:
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FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 09/119,995
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R
REGISTRATION UNMBER: 27,829
REFERENCE/DOCKET NUMBER: FJ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ
ADDRESSEE: THIBEAULT, LLP
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T: Severinov, Konstantin INVENTION: A CRYSTAL OF BACTERIAL CORE RNA POLYMERASE AND METHODS INVENTION: OF USE THEREOF
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SEKI, NORIAKI
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Pred. No. 2e+02
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RESULT 15
5180808-2
; Patent No. 5180808
; APPLICANT: RUOSLAHTI, ERKKI I.
; APPLICANT: RUOSLAHTI, ERKKI I.
; EQUENCES ENCODING THE SAME, NUCLEIC ACID PROBES, ANTI-VERSICAN ; ANTIBODIES, AND METHODS OF DETECTING THE SAME
; ANTIBODIES, AND METHODS OF DETECTING THE SAME
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION UNMBER: US/07/441,179
; SEQ ID NO:2:
; ETLING DATE: 27-NOV-1989
5180808-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 600-1-258
CURRENT APPLICATION NUMBER: US/09/396,651B
CURRENT FILING DATE: 199-09-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
SEQ ID NO 2
FEATURE: PATENTS AQUATICUS
FEATURE: PATENTS AGUATICUS
FEATURE: NAME/KEY: SITE
LOCATION: (695)..(696)
OTHER INFORMATION: Any amino acids can be at these two positions.
US-09-396-651B-2
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Search completed: October 11, 2001, 15:52:04 Job time: 207 sec
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Best Local Similarity 54.5
Matches 6; Conservative
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Best Local Similarity 55.6%;
Matches 5; Conservative
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Pred. No. 3.6e+02;
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Post-processing: Minimum Match
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is derived by analysis of the total score distribution.
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Match Length DB
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Gapop 10.0 , Gapext
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Best Local
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17_MOUSE
MK07_MOUSE
Q9WVS8;
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O1-OCT-2000 (Rel. 40, 0
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PROBABLE PROCESSING AND
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PRTP_HSVT2
                                                                                                                                                  EMBL; AF084543; AAD42934.1;
InterPro; IPR000501; -.
Pfam; PF01366; PRTP; 1.
Capsid assembly.
SEQUENCE: 782 AA; 87392 M
                                                                                                                                                                                                                                                                                              Bahr U., Springfeld C., Tidona C.A., Darai G.;
"Structural organization of a conserved gene cluster of Tupaia herpesvirus encoding the DNA polymerase, glycoprotein B, a probable processing and transport protein, and the major DNA binding protein.";
Virus Res. 60:123-136(1999).
-I- FUNCTION: THIS PROFEIN MAY AFFECT TRANSLOCATION OF THE VIRUS GLYCOPROTEINS TO MEMBRANES. IT IS INVOLVED IN CAPSID MATURATION
                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-99319892;
                                                                                                                                                                                                                                                                                                                                                                                              Herpesvirus tupaia (Strain 2) (THV-2). Viruses; dsDNA viruses, no RNA stage; Betaherpesvirinae.
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=132678;
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36 EQDIVETVGSR 246
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DYHC_HUMAN
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CYG3_HUMAN
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Pred. No.
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MAPK7 OR E
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Q13164; Q16634;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
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MITOGEN-ACTIVATED PROTEIN KINASE 7 (EC 2.7.1.-)
REGULATED KINASE 5) (ERK-5) (BMK1 KINASE).
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HSSP; P27703; 2ERK.
MGD; MGI:1346347; Mapk7.
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Mammalia; Eutheria;
                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                            MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                               Local Similarity
les 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is by non-profit institutions as long as its content is by non-profit institutions as long as its content is by non-profit institutions as long as its content is by non-profit institutions as long as its content is by non-profit institutions as long as its content is not removed. Usage by and for the content is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: THE SECOND PROLINE-RICH REGION MAY INTERACT WITH ACTIN TARGETING THE KINASE TO A SPECIFIC LOCATION IN THE CELL. PTM: AUTOPHOSPHORYLLATED ON THREONINE AND TYROSINE RESIDUES, WHITHE C-TERMINAL PART OF THE KINASE, WHICH COULD HAVE A REGULATOR
                                                                             3 EIDIIETIGN
| :||||||
4 EYEIIETIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS T
MAP KINASE SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                MGI:1346347; Mapk7.
rPro; IPR000719; -.
                                                                                                                                                                                                                                                                                                                                                                                PS01351; MAPK; 1
PS00107; PROTEIN_KINASE_ATP; 1
PS00108; PROTEIN_KINASE_DOM; 1
PS50011; PROTEIN_KINASE_DOM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IS ABSENT (BY SIMILARITY).
                                                                                                                                                                                                  908
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                       Serine/threonine-protein
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              STANDARD;
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                                                                                                                                                                                                                                                  347
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524
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Rodentia;
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kinase ERK5/BMK1 by r
d characterization of
                                                                                                                                                                                                                                                              PROTEIN KINASE.
PRO-RICH 1.
POLY-ARG.
PRO-RICH 2.
ATP (BY SIMILAR)
ATP (BY SIMILAR)
BY SIMILARITY.
                                                                                                                                 :
                                                                                                                                             Score 40; DB
Pred. No. 18;
                                                                                                                                                                                                                         PHOSPHORYLATION (ACTIVATES THE KINASE) (BY SIMILARITY).
PHOSPHORYLATION (ACTIVATES THE KINASE)
                                                                                                                                                                                                                (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Sciurognathi; Muridae;
              PRT;
                                                                                                                                                                                                  E7CC41C4BBDE0633 CRC64;
                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                             (BY SIMILARITY).
                                                                                                                                                                                                                SIMILARITY
              815
                                                                                                                                                                                                                                                                                                                                                                       kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                         بر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYROSINE RESIDUES, WHEN COULD HAVE A REGULATORY
                                                                                                                                 ATP-binding; Cell cycle;
                                                                                                                                                         Length 806;
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f a signaling pathway
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
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A Lee J.-D., Ulevitch R.J., Han J.;

A Lee J.-D., Ulevitch R.J., Han J.;

Primary structure of BMK1: a new mammalian map kinase.";

Biochem. Blophys. Res. Commun. 213:715-724(1995).

C -!- FUNCTION: MEX5 AND ERK5 INTERACT SPECIFICALLY WITH ONE A

CC NOT WITH MEK1/ERK1 OR MEK2/ERK2 PATHWAYS.

CC NOT WITH MEK1/ERK1 OR MEK2/ERK2 PATHWAYS.

CC PHOSPHORYLATION: ACTIVATED BY TYROSINE AND THREONINE

CC PHOSPHORYLATION (BY SIMILARITY).

CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY ADULT TISSUES. AB:

HEART, PLACENTA, LUNG, KIDNEY AND SKELETAL MUSCLE. NOT
                                                                                                                                                                                                                                                                               MBL;

MSSP; P249+...

MIM; 602521; -...

InterPro; IPR000719; -..

InterPro; IPR002290; -..

Pfam; pF00069; pkinase; 1.

PROSITE; PS01351; MAPK; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PS0011; PROTEIN_KINASE_DOM; 1.

**TORET ON THE OWNER OF THE OWNER OF THE OWNER 
                                                      NP_BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                               Phosphorylation DOMAIN 3
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01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation updat
MITCCEN-ACTIVATED PROTEIN KINASE 7 (EC 2.7.
REGULATED KINASE 5) (ERK-5) (ERK4) (BMK1 KI
MAPK7 OR PRKM7 OR ERK5 OR ERK4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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DOMAIN
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MEDLINE-95279403; PubMed-7759517;
Zhou G., Bao Z.O., Dixon J.E.;
"Components of a new human protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U29727;
HSSP; P24941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between
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                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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U29725; AAA82931.1;
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337
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; AAA82932.1;
; AAA82933.1;
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                                                                                                                                                                                                         POLY-ALA.
PRO-RICH 1.
                      ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (ACTIVATES THE
                                                                                                                                                         POLY-ARG.
PRO-RICH 2.
                                                                                                                                                                                                                                                                            PROTEIN KINASE
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7 (EC 2.7.1.
SIMILARITY).
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Best Local Similarity
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Matches 8
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15-DEC-1998 (
DNA-DIRECTED
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SEQUENCE
                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as 10nd as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch)
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01-FEB-1996
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                                                                                                                                                                      Transferase;
SEQUENCE 1:
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                                              2 GEIDIIETIGNR 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENZYME WHICH BETA' CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBSTRATES
                GEVDDIDHLGNR 486
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                                                                                                                                                                    PF00562; RNA_POL_B; 1.
TE; PS01166; RNA_POL_BETA;
ferase; Transcription; DNA-
NCE 1302 AA; 146533 MW;
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8; Conserv
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. 37, Last annotation update)
POLYMERASE BETA CHAIN (EC 2.
POLYMERASE BETA SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IS COMPOSED OF :
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88636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spiroplasma
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                                                                                                                                                                      DNA-directed RNA polymerase. MW; 8D971C23EB9FEB2F CRC64;
                                                                                  Score 40; DB Pred. No. 30; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40;
Pred. No.
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(BY SIMILARITY).
AREGREPRHRICLCS -> GPVKVEPAHTAASVA (IN
REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1302 AA
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gene is adjacent to rpoB.";
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                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
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                                                                                                                  Length 1302;
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RESULT 5
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P57146;
01-OCT-2000
                                                                                                                                                                                                        RPOB_BUCAP
P41184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A. MEDLINE-93160925; Pu Clark M.A., Baumann
                                                                              Buchnera aphidicola
Bacteria; Proteobac
                                                                                                                                           DNA-DIRECTED
                                                                                                                                                                                                                                          BUCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase;
SEQUENCE: 1
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Nature 407:81-86(2000).

-i-FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION

OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BETA CHAIN) (
RPOB OR BUO34
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01-OCT-2000
                                                                                                                                                           30-MAY-2000
                                                                                                                                                                          01-FEB-1995
                                                                                                                                                                                            01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01166; RNA_POL_BETA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP001118; BAB12761.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shigenobu S., Watanabe H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-TOKYO 1998;
MEDLINE-20445173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          symbiotic bacterium)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buchnera aphidicola (subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Buchnera
                                                              NCBI_TaxID=98794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome sequence of the endocellular bacterial symbiont of
                                                                                                                                                                                                                                                                                                       440
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BETA' CHAIN.
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                                                                                                                            CHAIN)
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                                                                                Proteobacteria;
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                                                                                                                                                           (Rel.
(Rel.
(Rel.
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(Rel. 40, Last annotation update)
D RNA POLYMERASE BETA CHAIN (EC 2.7.7.6)
(RNA POLYMERASE BETA SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription;
342 AA; 151467
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                                                                                                                           . 3), Last sequence update)
. 39, Last annotation update)
POLYMERASE BETA CHAIN (EC 2.7
POLYMERASE BETA SUBUNIT).
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                PubMed=1369199;
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58.3%;
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 Baumann
                                                                             gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                             TA; 1.

DNA-directed RNA polymerase.
MW; 95252459873DF940 CRC64;
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                                                                             Schizaphis graminum)
nmma subdivision; Buc
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31;
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                                                                                Buchnera
                                                                                                                                                                                                                                                                                                                                                                                               Length 1342;
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Best Loc
Matches
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21-JUL-1986
01-NOV-1997
region f
Nucleic
[3]
                                                                                                                                                                                                           MEDLINE-81260785; PubMed-6266829;
Ovchinnikov V.A., Monastyrskaya G.S., Gubanov V
Chertov O.Y., Modyanov N.N., Grinkevich V.A., M
Marchenko T.V., Polovnikova I.N., Lipkin V.M.,
"The primary structure of Escherichia coli RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpoB (beta-subunit of RNA polymerase) and portions Curr. Microbiol. 25:283-290(1992).

-1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZE OF DNA INTO RNA HSTMC THE TOTAL POLYMERASE CATALYZE
                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annottation update)
DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6) (TRANSCRIPTASE
BETA CHAIN) (RNA POLYMERASE BETA SUBUNIT).
RPOB OR GRON OR NITB OR RIF OR RON OR STL OR STV OR TABD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00562; RNA_POl_B: 1.
PROSITE; PS01166; RNA_POL_BETA;
Transferase; Transcription; DNA-
SEQUENCE 1342 AA; 152060 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                               "The primary structure of sequence of the rpoB gene
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                               "Analysis of the Escherichia coli
region from 89.2 to 92.8 minutes."
                                                                 Daniels D.L.;
                                                                                    Blattner
                                                                                                  STRAIN-K12 / MG1655;
MEDLINE-94089392; Pu
                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                   Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli
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                  Acids
                                                                                                                                                                  Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an email to license@isb-sib.ch).
                                                                               F.R.,
                                                                                                                                                                                                                                                                                                                                                                  Proteobacteria;
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                                                                                                                                   Z.A.
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                                                                                  Burland
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                                                                                                                                                                116:621-629(1981).
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                                                                               PubMed=8265357;
rland V.D., Plunkett
                 5 92.8 minutes.";
21:5408-5417(1993)
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HE FOUR RIBONUCLEOSIDE TRIPHOSPHATES
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, Makarova I.A.
., Sverdlov E.D
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[9]
SEQUENCE OF 187-1144 FROM N.A.
SPOTENCE OF 187-1144 FROM N.A.
Ovchinnikov Y.A., Sverdlov E.D., Lipkin V.M., Monastyrskaya G.:
Chertov O.Y., Gubanov V.V., Guryev S.O., Modyanov N.N.,
Grinkevich V.A., Makarova I.A., Marchenko T.V., Polovnikova I.
"Primary structure of RNA polymerase from E. coli; nucleotide
of EcoRl-C fragment of gene rpoB and amino acid sequence of the corresponding fragment of beta-subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
Sverdlov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLULINE-81165543; PubMed-7011900;
Delcuve G., Downing W., Lewis H., Dennis P.P.
"Nucleotide sequence of the proximal portion beta subunit gene of Escherichia coll.";
Gene 11:367-373(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gurevich A.I., Avakov A.E.
"The nucleotide sequence
Escherichia coli.";
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Miller E.
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Sverdlov E.D., Lipkin V.M.
Guryev S.O., Chertov O.Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [6]
SEQUENCE OF 1-188 FROM N.A.
Gurevich A.I., Avakov A.E.,
Gurevich at the sequence at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc.
                                                                "A beta subunit mutation disrupting the catalytic function of Escherichia coli RNA polymerase.";

Proc. Natl. Acad. Sci. U.S.A. 88:6018-6022(1991).

-i-FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCIOF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES
                                                                                                                                                  MUTAGENESIS OF GLU-813.
MEDLINE=91296752; PubMed=2068078;
Lee J., Kashlev M., Borukhov S.,
                                                                                                                                                                                                                                      Mollet C., Drancourt M., Raou
"RNA polymerase beta-subunit.
                                                                                                                                                                                                                                                                        STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                                          Gurevich A.I., Igoshin A.V., Kolosov M. "Structure of a central part of E.coli sequence of the gene for beta subunit o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bioorg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The nucleotide sequence of strong the E.coli rpoB structural gene."; Bloorg. Khim. 6:309-312(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the rpoB
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Monastyrskaya G.S.,
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the beta-subunit.";
m. 6:1423-1426(1980).
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m. 6:1580-1584(1980).
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D., Lipkin V.M., Monastyrskaya G
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                                                                           SEQUENCE FROM N.A.

Sverdlov E.D., Lisitsyn N.A., Guryev S.O., Monastyrskaya G.S.;

"Nucleotide sequence of the rpoB gene of Samonella typhimurium
for the beta-subunit of RNA polymerase.";

Dokl. Biochem. 287:62-65(1986).
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MEDLINE-89052707;
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. POLYMERASE BETA CHAIN (EC 2.7.7)
. POLYMERASE BETA SUBUNIT).
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LFENLE'S -> CSTCSSPT (IN REF. D -> V (IN REF. 1 AND 9).

MW; F9E95344C54ABBTA
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P43738;
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"Genes coding for RNA polymerase beta
structure/function analysis.";
Eur. J. Biochem. 177:363-369(1988).
[3]
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InterPro; IPR001572; -.
Pfam; PF00562; RNA_pol_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-slb.or send an email to license@isb-sib.ch).
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                  STRAIN-RD / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D. Adams M.D., Whi
Kerlavage A.R., Bult C.J., Tomb J
                                                                                                                                                                                              RPOB OR HI0515.
Haemophilus influenzae.
Bacteria; Proteobacteri
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PROSTIE; PS01166; RNA_POL_BETA; 1.
Transferase; Transcription; DNA-directed RNA polymerase.
CONFLICT 401 401 G -> A (IN REF. 3).
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EMBL; M38311; AAA27215.1;
PIR; S01794; RNEBBT.
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Bioorg. Khim. 12:699-707(1986).
-i-FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                           SEQUENCE
                                                                                                                                                   NCBI_TaxID=727;
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POLYMERASE BETA SUBUNIT).
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150557 MW;
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                  M.D., White
J., Tomb J.-I
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Fitzhugh
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Dougherty B ields C.A., (
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                    Clayton R.A., Kirkness E.
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RPOB OR NMA0142.
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InterPro; IPRO01572; -.
Pfam; PF00562; RNA_POL_B; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
Transferase; Transcription; DNA-directed RNA
Transferase; Transcription; DNA-directed RNA
Transferase; Transcription; DNA-directed RNA
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the Euro
                                        STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE-2022556; PubMed-10761919;
Parkhill J. Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Bavies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd
Jayels K., Leather S., Moule S., Mungall K., Quall M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
menigitidis 22491."
"menigitidis 22491."
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-I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
-I- FUNCTION: DNA FIGTMG THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
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01-OCT-2000
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Venter J.C.;
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Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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Weidman J.F., Phillips C.
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                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      Neisseria meningitidis (serogroup
Bacteria; Proteobacteria; beta sul
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                                                                                                                                                                                                                        NCBI_TaxID=65699;
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                           Nature 404:502-506(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Whole-genome random sequencing influenzae Rd.":
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440 GEVDDIDHLGNR 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content ified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBSTRATES.
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               FUNCTION: DNA-DEPENDENT RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BETA' CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENZYME WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA(N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEIDIIETIGNR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                           (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                           (Rel. 40, Created)
                                                                                                                                                                                                                                                                                 (RNA POLYMERASE
                                                                                                                                                                                                                                                                                                                (Rel.
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                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                 . 40, Last sequence update)
. 40, Last annotation update)
POLYMERASE BETA CHAIN (EC 2.7,
POLYMERASE BETA SUBUNIT).
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58
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                                                                                                                                                                                                                                      erogroup A).
beta subdivision;
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Pred.
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 FOUR
POLYMERASE CATALYZES THE TRANSCIOUR RIBONUCLEOSIDE TRIPHOSPHATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.;
                                                                                                                                                                                                                                                                                                                                                                         1392 AA
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31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGMA CHAIN AND THE CHAINS, 1 BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                        Neisseriaceae;
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             THE TRANSCRIPTION
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RESULT 11
RPOB_NEIMB
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                               Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Elsen J.A., Ketchum K.A., Hood D.W., Peden J.E., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Mouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPOB_NEIMB
Q59622;
                                                                                  MC58.";
Science 287:1809-1815(2000).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                              STRAIN-MC58
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   Nolte
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Bacteria; Proteobacteria; beta sul
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-DIRECTED
BETA CHAIN) (
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01-OCT-2000
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                                           <del>:</del>
                                                                                                                                       MC58.";
                                                                                                                                                                                                                                                                            STRAIN-MC58 / SEROGROUP B;
MEDLINE-20175755; PubMed-10710307;
                                                                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                                               STRAIN-BNCV / SEROGROUP
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01166; RNA_POL_BETA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=491;
                                                                                                                                                      'Complete genome sequence of Neisseria meningitidis serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 GEVDDIDHLGNR 478
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- CATALYTIC A
RNA(N).
RNA(N).
SUBUNIT: THE ENZYME WHICH BETA' CHAIN.
SIMILARITY: B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: THE ENZYME WHICH
                                                                     CATALYTIC ACTIVITY: N
                                                                                                                                                                                                                                                                                                                                                   0.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL162752; CAB83457.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conserv
                                                                                                                                                                                                                                                                                                                                     (OCT-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 35, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
D RNA POLYMERASE BETA CHAIN (EC 2.7.7.
(RNA POLYMERASE BETA SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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  BELONGS
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                                           ENZYME
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                           COMPOSED OF
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58.3%;
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                                                                      NUCLEOSIDE TRIPHOSPHATE -
                                                                                                                                                                                                                                                                                                                                                                                                                      beta subdivision; Neisseriaceae; Neisseria
  THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-directed RNA polymerase. MW; BA4AF438619CB82C CRC64;
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Pred. No.
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  RNA POLYMERASE
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                                           OF,
                           OF THE
ALPHA
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32;
                           SIGMA CHAINS,
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  BETA
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                                                                      N PYROPHOSPHATE
                                                                                                             TRANSCRIPTION
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RESULT 12
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Best Local
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01-OCT-1996
01-OCT-1996
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                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
NUCLEOPORIN NUP188 (NUCLEAR PORE PROTEIN NUP188).
                                                                                                                                                                                                                                                                                 N188_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase;
CONFLICT
                     STRAIN-S288C / AB972;
Devlin K., Churcher C.,
Submitted (AUG-1994) to
                                                                                      SEQUENCE FROM N.A.
Nehrbass U., Rout
                                                                                                                       SEQUENCE FROM N.A. Zabel U., Doye V., Te Submitted (JAN-1996)
                                                                                                                                                                                                               NUP188 OR YML103C
                                                                                                                                                                                                                                                                        P52593;
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PROSITE; PS01166; RNA_POL_BETA;
                                                                                                                                                                   NCBI_TaxID-4932;
                                                                                                                                                                                Saccharomycetales;
 SEQUENCE OF 1187-1205 AND 1611-1629
                                                      SEQUENCE FROM N.A
                                                                              Submitted
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AE002371; AAF40591.1; ALT_INIT.
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                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                           U., Rout M.P., (FEB-1996) to
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818
836
1190
1201
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1373
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378
648
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                                                                                                                                  Tekotte H.,
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360
378
648
706
718
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58.3%;
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                      the
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                                                                                      Maguire S.,
                                 Barrell B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                       VP -> SA (IN REF. 1).

GG -> A (IN REF. 1).

F -> L (IN REF. 1).

GY -> VN (IN REF. 1).

YNG -> SR (IN REF. 1).

A -> S (IN REF. 1).

DDP -> EDA (IN REF. 1).

F -> L (IN REF. 1).

F -> L (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-directed RNA polymerase
N -> S (IN REF. 1).
L -> I (IN REF. 1).
                                                                                                                        H., Wepf R., Hurt E.C.; EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                            XX:
                      EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                     Ψ
                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                              Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISSING (IN REF. 1).
A -> G (IN REF. 1).
A -> P (IN REF. 1).
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RNVLFVFKRCSNRFGRRPSES (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AYISHTLETDE -> VISPIPCVRMK (IN REF. 1).
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                                                                                       Blobel G.,
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                                 Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                Saccharomyces.
                                                                                                                        databases
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                      databases
                                                                              databases
                                                                                       Wozniak R.W.;
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RESULT 13
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Best Local
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Altchison J.D., Rout M.P., Marchin M., Blobel G., Wozniak R.W.;
"Two novel related yeast nucleoporins nupl70p and nupl57p:
complementation with, the vertebrate homologue Nupl55p and funct:
interactions with the yeast nuclear pore-membrane protein Pom15:
J. Cell Biol. 131:1133-1148(1995).

-i- FUNCTION: INTERACTS WITH THE CORE STRUCTURE OF THE NUCLEAR COMPLEX (NPC). MAY PROVIDE THE NECESSARY ASYMMETRY REQUIRED ANCHORING STRUCTURES SUCH AS CYTOPLASMIC FILAMENTS AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GUB_RHOMR
P45798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
BETA-GLUCAMASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCAMASE)
(1,3-1,4-BETA-D-GLUCAN 4-GLUCANOHYDROLASE) (LICHENASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1290 SGEIDFIKNIG 1300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X90580; CAA62208.1; -. EMBL; U47107; AAA88904.1; -. EMBL; X80835; CAA56794.1; -.
                                                                   This
                                                                                                   -I- FUNCTION: SHOWS ACTIVITY ON LICHENAN, BETA-GLUCAN AND LAMINARIN BUT NOT ON CMC CELLULOSE OR XYLAN. THE ENZYME HAS A TEMPERATURE OPTIMUM OF 85 DEGREES CELSIUS AND A PH OPTIMUM OF 7.0.
-I- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-BETA-D-GLYCOSIDIC LINKAGES IN BETA-D-GLUCANS CONTAINING 1,3- AND 1,4-BONDS.
-I- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                Spilliaert R., Hreggvidsson G.O., Kristjansson J.K., Eggertsson G. Palsdottir A.; "Cloning and sequencing of a Rhodothermus marinus ge for a thermostable beta-glucanase and its expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                         between the Swiss Institute or Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                MEDLINE-95010084; PubMed-7925416;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=29549;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Rhodothermus marinus
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                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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8; Conserv
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AA; 188576 MW;
                                                                                                                                                                                                               224:923-930(1994)
                                                                                                                                                                                                                                                                                                                                                                                                          Rhodothermus group; Rhodothermus
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Pred. No.
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                There are no restrictions ng as its content is in
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Matches 7
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01-FEB-1996
15-DEC-1998
15-DEC-1998
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SEQUENCE
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Hydrolase;
SIGNAL
CHAIN
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Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
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                     InterPro;
Pfam; PF00
                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIR-ATCC 10231;
MEDLINE-93657593; PubMed-8771707;
Stoldt V., Rademacher F., Kehren V., Er
"Revlew: the Cct eukaryotic chaperonin
cerevisiae and other yeasts.";
Yeast 12:523-529(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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HSSP; P23904;
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                                                           InterPro;
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                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.
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                                                                                                                      s requires a license agreement (S an email to license@isb-sib.ch).
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PS01034; GLYCOSYL_HYDROL_F16;
PS00750; TCP1_1;
                                      IPR002194;
IPR002423;
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98 (Rel. 37, Last sequence update)
98 (Rel. 37, Last annotation update)
PROTEIN 1, THETA SUBUNIT (TCP-1-T
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163
286
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286
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PROTON DONOR (BY SIMILARITY);
7215C33624135191 CRC64;
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(TCP-1-THETA)
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in subunits of Saccharomyces
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Pfam; PF00914; CNG_membrane; 1.

Pfam; PF00917; CNMP_BINDING_1; 1.

R Pfam; PF00927; CNMP_BINDING_1; 1.

R PROSITE; PS00888; CNMP_BINDING_2; 1.

PROSITE; PS00889; CNMP_BINDING_2; 1.

PROSITE; PS50042; CNMP_BINDING_3; 1.

PROSITE; PS50042; CNMP_BINDING_2; 1.

PROSITE; PS50042; CNMP_BINDING_2; 1.

PROSITE; PS00089; CNMP_BINDING_2; 1.

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Q24278;
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MEDLINE-95045396; PubMed-7957070;

Baumann A., Frings S., Godde M., Seifert R., Kaupp U.B.;

Baumann A., Frings S., Godde M., Seifert R., Kaupp U.B.;

Primary structure and functional expression of a Drosophila cyclic nucleotide-gated channel present in eyes and antennae.";

EMBO J. 13:5040-5050(1994).

-I- FUNCTION: APPROXIMATELY 50-FOLD MORE SENSITIVE TO CGMP THAN TO CAMP. MAY BE INVOLVED IN TRANSDUCTION CASCADES OF BOTH INVERTEBRATE PHOTORECEPTORS AND OLFACTORY SENSILLAE.

-I- TISSUE SPECIFICITY: EXPRESSED IN ANTENNAE AND THE VISUAL SYSTEM.

-I- SINILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
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PROSITE; PS00995; TCP1_3; FALSE_NEG.
Chaperone; ATP-binding; Multigene family.
SEQUENCE 540 AA; 58918 MW; F962285DA6EB03DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL (CNG CHANNEL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMRI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
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Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0014462;
InterPro; IPR000595;
InterPro; IPR002025;
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ALIGNMENTS

Query Match Best Local Matches 077072 PRELIMINARY; 077072; 01-NOV-1998 (Tremblrel. 08, Cr 01-NOV-1998 (Tremblrel. 08, La 01-NOV-1998 (Tremblrel. 08, La COELOMIC CYTOLYTIC FACTOR 1. SEQUENCE FROM N.A. MEDLINE-98406152; PubMed-9733802; MEDLINE-98406152; PubMed-9733802; MEDLINE-98406152; PubMed-9733802; MEDLINE-98406152; PubMed-9733802; MEDLINE-98406152; PubMed-9733802; MEDLINE-98406152; Name of Elsenia For Battelier P., Timmermans M.; "Identification and cloning of a glucan- and lipopolysaccharidebinding protein from Elsenia foetida earthworm involved in the activation of prophenoloxidase cascade."; J. Biol. Chem. 273:24948-24954(1998). EMBL; AF030028; AAC35887.1; EMBL; AF030028; AAC35887.1; EMBL; AF030028; AAC35887.1; Eisenia foetida (Common brandling worm) (Eukaryota; Metazoa; Annelida; Clitellata; Lumbricina; Lumbricidae; Eisenia. 178 NCBI_TaxID=6396; CCF1 1 SGEIDIIETIGNR 13 SGEIDIIETIGNR 190 al Similarity 13; Conservati 100.0%; Score 64; DB 5; ilarity 100.0%; Pred. No. 0.0028; Conservative 0; Mismatches 0 Last sequence update) Last annotation update) Created) PRT; 384 (Common dung-worm). ₿ Oligochaeta; Haplotaxida; Length 384; Indels 0; Gaps

Q51333; Q51333; Q1-NOV-1996 Q1-NOV-1996 Q1-MAY-2000

(TrembLrel. 01, 05 (TrembLrel. 01, 1) (TrembLrel. 13, 1

Created)

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InterPro; IPR000757;
InterPro; IPR000757;
Pfam; PF00722; Glyco_hydro_16; 1.
PPASTIE; PS01034; GLYCOSYL_HYDROL_F16; 1.
PASTIE; PS01034; 32835 MW; CD8DB8ClA6F8DC04 CRC64;
PASTIE; PS01034; 32835 MW; CD8DB8ClA6F8DC04 CRC64;
PASTIE; PS01034; 32835 MW; CD8DB8ClA6F8DC04 CRC64;
                                                                                                                               Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ferrer P., Halkier T., Hedegaard L., Savva D., Diers I., Asenjo "Nucleotide sequence of a beta-1,3-glucanase isoenzyme IIA gene Oerskovia xanthineolytica LL G109 (Cellulomonas cellulans) and i
                                                                                                                                                          Lee S., Wang R., Soderhall K.;

"A lipopolysaccharide and beta-1,3-glucan-binding protein from hemocytes of the freshwater crayfish Pacifastacus leniusculu: purification, characterization, and cDNA cloning.";

J. Biol. Chem. 275:1337-1343(2000).
                                                                                                                                                                                                                              SEQUENCE FROM N.A. TISSUE-HEMOCYTES;
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Actinomycetales; Micro
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                                                                                                                                                                                                                  MEDLINE=20092910; PubMed=10625682;
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Eumalacostraca; Euca
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HSSP; P23904;
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MEDLINE-96345651; PubMed-8755914;
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AAC44371.1; -.
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Eucarida; Decapo
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BETA-1,3-GLUCAN BINDING PROT
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Decapoda; Pleocyemata; Astacic
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2; Mismatches
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Pred. No.
                                                                                              LIPOPOLYSACCHARIDE AND BINDING PROTEIN.
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007242;
01-JUL-1997 (TrE
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PROBABLE BETA-1,
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PROSITE; P
SEQUENCE
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Q26660;
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Bacteria; Firmicutes; Actin
Actinomycetales; Corynebact
                                                                                                            "Molecular cloning of the first metazoan beta-1,3 of the sea urchin Strongylocentrotus purpuratus.", Proc. Natl. Acad. Sci. U.S.A. 93:6808-6813(1996).
EMBL; U49711; AAC47235.1; -
SEQUENCE 499 AA; 55274 MW; D863F36EEOCFF5AC CF
                                                                                                                                                                                                                                                                                                                                                                Strongylocentrotus purpura
Eukaryota; Metazoa; Echino
Echinoidea; Euechinoidea;
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NCBI_TaxID=7668;
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294 AA; 32186 MW; 7B9897BA6740BEB0
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noidea; Echinacea;
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Score 45; DB pred. No. 9.5; 3; Mismatches
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1; Echinoida; Strongylocentrotidae;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteric
Bacteria; Firmicutes; Actinobacteria; Actinobacteric
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EMBL: AL445945; CAC14352.1; ...
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Cerdeno A.M.,
                                                                                                                                                   Enzyme Microb.
                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-LL G109;
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NCBI_TaxID=1902;
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                                 MEDLINE-96409238; PubMed-8814220;
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NCBI_TaxID-1826;
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permeabilize the yeast cell wall.";
Ann. N. Y. Acad. Sci. 782:555-566(1996).
                                                               the 8 Mb Streptomyces coelicolor Mol. Microbiol. 21:77-96(1996). EMBL; AL450165; CAC16455.1; -.
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Pfam; PF00722; Glyco_hydro_16; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
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MW;
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e EMBL/GenBank/DDBJ databa
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IT IPOB GENE SEQUENCING.";

L. SUDMILTER (JUL-1999) to the EMBL/GenBank/DDBJ databases.

C. I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION

C. OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS

C. SUBSTRATES (BY SIMILARITY).

C. I- ATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +

C. I- RNA(N) (BY SIMILARITY).

C. I- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.

BE HBL; AF165994; AAF80850.1;

R Interpro; IPRO01572;

R POSITE; PS01166; RNA_POL_BETA; 1.

DNA-directed RNA POLYMETASE; Transcription; Transferase.

SEQUENCE 1383 AA; 154780 MW; 9B007A67C872498E CRC64;
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Bacteria; Proteobacteria; alpha subdivision
Bartonellaceae; Bartonella.
SEQUENCE FROM N.A.
STRAIN-HOUSTON-1;
STRAIN-HOUSTON-1;
Renesto P., Gouvernet J., Dra
"New approach to identifying
rpoB gene sequencing.";
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                                                                                                                                                                                           Bartonellaceae; B
NCBI_TaxID=38323;
                                                                                                                                                                                                                                                          Bartonella henselae (Rochalimaea henselae).
Bacteria; Proteobacteria; alpha subdivision;
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InterPro; IPR002049; -...
PRINTS; PR00011; EGFLAMNIN.
PROSITE; PS00022; EGF_1; UNKNOWN_2.
PROSITE; PS01186; EGF_2; 2.
EGF-11ke domain; Glycoprotein; HypothseQuence 736 AA; 84202 MW; 349E0F
Q9F406;
Q9F406;
01-MAR-2001
01-MAR-2001
01-MAR-2001
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Q9SVX7;
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Eukaryota; Viridiplantae; Embryophyta; Trachec
Magnoliophyta; eudicotyledons; core eudicots;
Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Pfam; PF00562; RNA_POL_B; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
DNA-directed RNA polymerase; Transcription; Transferase.
SEQUENCE 1383 AA; 154852 MW; 2CEE87E06A3207B6 CRC64;
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01-MAY-2000 (TIEMBLITEL 13, La-
01-MAR-2001 (TIEMBLITEL 16, La-
01-MAR-2001 (TIEMBLITEL 16, La-
HYPOTHETICAL 84.2 KDA PROTEIN.
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-!- SIMILARITY: BELONGS TO EMBL; AF171070; AAF87049.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
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Submitted (JUN-1999) to the
EMBL; AL049660; CAB41192.1;
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Mayer K.F.X., Lemcke K
Submitted (APR-1999) to
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STRAIN-B:4:P1.10;
Stefanelli P., Fazio C.,
Mastrantonio P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stefanelli P., Fazio C., La Rosa
Mastrantonio P.;
                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-B:14:P1.12,
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of point
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPOB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ270502; CAC14806.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or point mutations in the the strain.";
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Neisseria meningitidis.
Bacteria; Proteobacteria;
NCBI_TaxID=487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Rifampin-resistant meningococci causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria;
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    Antimicrob. Chemother. 0:0-0(0).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the strain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rifampin-resistant meningococci causing invasive
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GEVDDIDHLGNR
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                                                                                                                                                                                                                                                                                                                                                  AJ270504; CAC14808.1;
AJ270500; CAC14804.1;
AJ270503; CAC14807.1;
                                                                                                                 Similarity 58.: 7; Conservative
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7; Conservative
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342 AA;
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342 AA;
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L (TrEMBLIEL. 16, 1
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37264 MW;
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37253 MW;
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58.3%;
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58.3%;
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3a G., 1
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*

2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*

3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
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                                                                                                                                                                       /SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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/SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                     /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Result
10087654021	
2240 350 350 340.5 314 314 310 296 286.5 209 208	1
100.0 15.6 15.6 14.0 14.0 13.8 13.8 12.8 9.3	% Query Match
384 435 263 457 261 422 673 233	% Query Match Length DB
18 18 18 17 17 17 16	BB
AAW29457 AAW29456 AAW29456 AAW29455 AAR89136 AAR89137 AAR11599 AAR91362 AAW56275 AAR67915 AAR67918	SUMMARIES
Eisenia foetida co Oerskovia xanthine Oerskovia xanthine Oerskovia xanthine Bombyx mori mature Bombyx mori full l Beta-1,3-glucanase Oerskovia beta-1,3 Flavobacterium ker (1-3)-beta-D-gluca	Description

45	44	43	42	41	40	39	38	37	36	35	ω 4	ü	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	
96	96	96	96	96	98.5	98.5	99	100	100.5	101.5	101.5	101.5	102.5	102.5	102.5	103	103	105	105	107	107.5	108	111	111	111	111.5	112.5	112.5	113.5	121.5	131.5	138.5	168.5	
4.3	4.3	4.3	4.3	4.3	4.4	4.4	4.4		4.5				4.6	4.6	4.6	4.6	4.6	•			٠	4.8	٠						٠					
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AAG36454	AAG43412	AAG36455	AAG43413	AAG36456	AAW93001	AAR06621	AAY54011	AAR06622	AAG48467	AAG11993	AAG11994	AAG11995	AAG52470	AAG52471	AAG52472	AAG40081	AAG40082	AAG07535	AAG07536	AAB63197	AAW50908	AAG32464	AAG18642	AAG18643	AAG18644	AAR13993	AAB48550	AAR20192	AAW34987	AAW77311	AAR88406	AAB52463	AAW92310	
	Arabidopsis thalia	Arabidopsis thalia		Arabidopsis thalia	B. alkalophilus be	Hybrid (1,3-1,4)-p	Amino acid sequenc	Hybrid (1,3-1,4)-p	. Arabidopsis thalia										Arabidopsis thalia	Gene 21 human secr	н				Arabidopsis thalia	 A.altocetigenes me 	Ruminococcus flave	ADH complex protei	Bankia gouldi endo	Phaffia rhodozyma	Trichoderma harzia	m tub	Streptomyces sp. S	

ALIGNMENTS

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RESULT AAY24914
De Baetselier P;
                                                17-DEC-1997;
                                                                                          24-JUN-1999.
                                                                                                               W09931229-A2.
                                                                                                                                                                                               Eisenia foetida.
                                                                                                                                                                                                                  trypanosomal infection; b inflammation; immunology.
                                                                                                                                                                                                                           Eisenia foetida; coelomic cytolytic factor 1; CCF-1; cancer; trypanosomal infection; bacterial infection; tumour therapy;
                                                                                                                                                                                                                                                         Eisenia foetida coelomic cytolytic factor 1 protein.
                                                                                                                                                                                                                                                                             25-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                    AAY24914;
                                                                                                                                                                                                                                                                                                                      AAY24914 standard; Protein; 384 AA
                             (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG
                                                                     16-DEC-1998;
                                                                                                                                             Protein
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                                                 97EP-0203974.
                                                                     98WO-EP08169.
                                                                                                                                 /label= signal
18..384
/label= CCF-1
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1999-385905/32

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                        Oerskovia xanthineolytica beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
             Beta-1,3-glucanase; lytic enzyme; yeast; beta glucan degradation; fungal cell wall; intracellular product; purification; protoplast
                                                                                                                                              AAW29457 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GANSFYRDGKLFIKPTLLADNINPQTGAPFGTDEMYNGYLDVWAMYGACTNTDNNGCYRT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRWTLVVLCLLFGEGFAFTDWDQYHIVWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQD
                                                                                                                                                                                                                   KWTWDDEGDNNAMQVDYIRVYKRN 384
                                                                                                                                                                                                                                                                                                                                                                                                LAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNW 360
                                                                                                                                                                                                                                                                                                                                      FWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                          gaagdippamsarvrtiqkysithgrvvvhakmpvgdwlwpaiwmlpedwvyggwprsge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gansfvrdgklfikptlladninpqtgapfgtdfmyngvldvwamygactntdnngcyrt
                                                                                                                                                                                                                                                                                                                                                                                                                               IDIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   foetida polypeptides derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 48-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                     (first
                                                                                                                                              Protein;
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Pred. No. 1.2e-204;
); Mismatches 0;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   prepare protoplasts studies.
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extracts, pharmaceuticals, food or feed compositions, and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated beta-1,3-glucanase enzyme xanthineolytica, used particularly for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-526451/48
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12-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 42-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for obtaining desirable products
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                                                                                        132
261 LLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTN 320
                              188
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                                                                                                        SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL:||: ::| | :|| :| :| :| :| :| :|
                                                                                                                                                                                                                              IVWQDEFDYFDG-----AKWQHEVTATGGGNSEFQLYTQDGANSFYRDGKLFIKPTLLAD
                            -----tvh-gpgysggs-gitgmyqhpqgwsfadtfhtfavdwkpgeitwfvd--gqq
                                              GIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQA
                                                                                       qpqygrieariqiprgqgiwpafwmlggsfpgtpwpssgeidimenvgfephrvhg----
                                                                                                                                                                                     NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
                                                                                                                                                                                                              llwsdefdgaagsapnpavwnhetgahgwgnaelqnytasransal-dgq-----
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96DK-0000427
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                                                                                                                                                                                                                                                                                          15.6%;
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                                                                                                                                                                                                                                                                            30;
                                                                                                                                                                                                                                                                          Score 350; DB 18;
Pred. No. 3.1e-25;
0; Mismatches 96;
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he lysis of microbial cells
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                                                                                                                                                                                                                                                                            96;
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                                                                    C This sequence comprises the polypeptide precursor of a novel C Oerskovia xanthineolytica enzyme that exhibits beta-1,3-glucanase C (BG) activity and which includes a mannose binding domain (MBD). C Its amino acid sequence was deduced from an isolated genomic DNA c sequence (see AAT89156). Claimed DNA constructs that encode the novel BG lacking a MBD (see AAW29455 and AAW29457), a MDB (see CAW29458), or the full-length enzyme can be used to produce recombinate BG polypeptides, with or without a mannose binding domain, in fungal consolidation or modification of beta-glucan containing material, corporated by the gentle lysis of microbial cell walls, thereby enabling recovery of desirable intracellular products with a reduced amount of contaminants. They can also be used for the
                                    production of e.g. pigments, colourants, flavourants, yeast extracts, pharmaceuticals, food or feed compositions, and t
                                                                                                                                                                                                                                                                                                                                                                                                             xanthineolytica, used particular
for obtaining desirable products
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12-APR-1996;
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fungal cell wall; intracellular product;
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DB; AAT89156.
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                                                                                                                                                                                                                                                                                                                                                                      Page 39-40; 64pp; English.
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96DK-0000427.
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    obtained from Oerskovia
the lysis of microbial cells

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purification; protoplast.
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Query Match
Best Local
Diers I,
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fungal cell wall; ir
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                                 (NOVO ) NOVO-NORDISK AS.
                                                                   23-AUG-1996;
12-APR-1996;
                                                                                                                                                       23-OCT-1997.
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                                                                                                                                                                                                                                                                                                                                                           Oerskovia xanthineolytica LLG109 (DSM 10297).
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                                                                                                                     14-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTN 320
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Ferrer P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                   96DK-0000885
96DK-0000427
                                                                                                                     97WO-DK00160
                                                                                                                                                                                                                                     /*tag= a
23..120
/*tag= b
164..952
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                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             e; lytic enzyme;
intracellular pr
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Halkier
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Pred. No. 4.9e-25;
                                                                                                                                                                                                                                                                                                                                                                                           p; yeast; beta glucan degradation;
product; purification; protoplast
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Hedegaard
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RESULT
AAR89136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW29458) or a full-length enzyme, i.e. BG with mannose binding domain (see AAW29456), can be used to produce recombinant BG polypeptides, with or without a mannose binding domain, in fungal or bacterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, especially for the gentle lysis of microbial cell walls, thereby enabling recovery of desirable intracellular products with a reduced amount of contaminants. They can also be used for the production of e.g. pigments, colourants, flavourants, yeast extracts, pharmaceuticals, food or feed compositions, and to prepare protoplasts for use in fusion, transformation and cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This polypeptide comprises a novel Oerskovia xanthineolytica (OX) enzyme that exhibits beta-1,3-glucanase (BG) activity. Its amino acid sequence was deduced from an isolated genomic DNA sequence (see ANT89155). Claimed DNA constructs that encode the novel BG also ANW29456 for corrected sequence), a mannose binding domain (AAW29458) or a full-length enzyme, i.e. BG with mannose binding
           Bombyx mori mature LPS-binding protein
                                            22-AUG-1996
                                                                                                        AAR89136 standard; protein; 455 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated beta-1,3-glucanase enzyme - obtained from Oerskovia xanthineolytica, used particularly for the lysis of microbial cells for obtaining desirable products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-526451/48
N-PSDB; AAT89155.
                                                                            AAR89136;
                                                                                                                                                                                                                    381
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                                                                                                                                                                                                                                                                               GFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                llwsdefdgaagsapnpavwnhetgahgwgnaelqnytasransal-dgg------
                                                                                                                                                                                                                                                                                                                                                                                                        GIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                     qpqygrleariqiprgqgiwpafwmlggsfpgtpwp-sgeidimenvgfephrvhg----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103;
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                                          (first entry)
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28.5%;
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                                                                                                                                                                                                                                                                                                            ----vfdqpfflilnvavggqw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 340.5;
Pred. No. 2e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5; DB 18;
2e-24;
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                                                                                                                                                                                                                                                --qqmkvdyvrv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacter cloacae strain 57-9. Partial amino acid sequence was used to generate PCR primers (AAT10280-1). These amplified a fragment of the gene used as a probe to obtain the full length gene (AAT10879) by screening a cDNA library derived from B.mori previously injected with heat-Killed E.cloacae. The protein or fragments of it, can be used to treat diseases associated with LPS complexes e.g. septic shock, to remove LPS from products used for injection and to protect transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding protein from Bombyx mori. The protein was isolated haemolymph of fifth stage B.mori larvae after injection with Enterobacter cloacae strain 57-9. Partial amino acid sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 41-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lipopoly-saccharide - esp
encoding it, for producing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lipopolysaccharide binding protein; Bombyx mori; haemolymph; primer; Enterobacter cloacae; PCR; polymerase chain reaction; amplification; probe; LPS complex; septic shock; injection; transgenic plant; vine; tobacco; tomato; potato; fungal infection; fungus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of a mature lipopolysaccharide (LPS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New protein from Bombyx mori that binds bacterial lipopoly-saccharide – esp. used to treat septic :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-060094/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUN-1994;
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Modified-site
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 315
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                                                                                                                                                                                                                                                                                                                                          27 VWQDEFDYFDGAKWQ-HEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLADNINPQ 85
AVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRK----FFDARGNWKWTWDDEGDN 370
                                                                   DDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNV 314
                                                                                                                                       GGEFLGIQKMGSTMHWGPGWD-DNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFV
                                                                                                                                                                                                          HGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWP-RSGEIDIIETIGN-----RDFKNT 195
                                                                                                                                                                                                                                          qhmpgflddsiysgtln---lfsgctss-aeacikqasgadilppivsgri-tsigfaft
                                                                                                                                                                                                                                                                            TGAP-FGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDI-PPAMSARVRTFQKYSFT 143
                                                                                                                                                                                                                                                                                                            ifeeqfdsldenvwqieqyipiyhpeypfvsyqrnnltvstadgnlhi----naklq 187
                                                                                                    ------vlyggpimdlecrenflstkrrrdgtswgdsfhtysvgwtpdfialsv
                                                                                                                                                                        ygtveiraklpqgdwlypeillepflkkygsmnyasgvvkiacargnaelysgpndysnt
                                                                                                                                                                                                                                                                                                                                                                                  101;
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                                                                                                                                                                                                                                                                                                                                                                                                14.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tomato or potato, against fungal infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              esp. used to treat septic shock, also sing transgenic plant(s) resistant to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "putative N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                58;
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                                                                                                                                                                                                                                                                                                                                                                              Score 314; DB 17;
Pred. No. 1.4e-21;
58; Mismatches 143
                                pavcahaprhllqagsqmapfddhfy1tlgv
                                                                                                                                                                                                                                                                                                                                                                                  143;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 455,
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17;

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RESULT
AAR89137
ID AAR8
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AC AARE
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DT 22-4
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KW 111pc
KW 211pc
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             Query Match
Best Local
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                                                                                        This is the amino acid sequence of the full length lipopolysaccharide (LPS) binding protein from Bombyx mori. The protein was isolated from the haemolymph of fifth stage B.mori larvae after injection with Enterobacter cloacae strain 57-9. Partial amino acid sequence was used to generate PCR primers (AAT10280-1). These amplified a fragment of the gene used as a probe to obtain the full length gene by screening a cDNA library derived from B.mori previously injected with heat-killed E.cloacae. The protein or fragments of it, can be used to treat diseases associated with LPS complexes e.g. septic shock, to remove LPS from products used for injection and to protect transgenic plants e.g. vines, tobacco, tomato or potato, against fungal infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lipopolysaccharide binding protein; Bombyx mori; haemolymph; primer; Enterobacter cloacae; PCR; polymerase chain reaction; amplification; probe; LPS-complex; septic shock; injection; transgenic plant; vine; tobacco; tomato; potato; fungal infection; fungus.
                                                                                                                                                                                                                                                                                                         New protein from Bombyx mori that binds bacterial lipopoly-saccharide - esp. used to treat septic shock, also DNA encoding it, for producing transgenic plant(s) resistant to fungal
                                                                                                                                                                                                                                                                  Claim 5; Page 42-43; 53pp; French
                                                                                                                                                                                                                                                                                                                                                                                                         Brey PT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUN-1994;
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                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bombyx mori full length LPS-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397
              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaggitef-rdgsitsgg---vtkpw----rdsarkasvhfwrhmsdwfprwsqp---
101;
                                                                                                                                                                                                                                                                                                                                                                   AAT10279
                                                                                                                                                                                                                                                                                                                                                                                                            Lee W;
                                                                      467
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94FR-0007083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94FR-0007083
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182
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13..46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
             14.0%;
27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "putative N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "mature protein"
58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467
           Score 314; DB 17;
Pred. No. 1.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
Mismatches
                           DB 17;
                                                                                                                                         can be used to treat diseases
143;
                        Length 467;
Indels
; 83
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443
17;
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AAR11599
ID AAR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                      The new enzyme is derived from alkaoplhilic Bacillus Sp. The enzyme acts on beta-1,3-glucans to form glucose and laminaribiose It is stable over a wide pH range with opt. activity at weakly actidic pH and has good heat resistance.
                                                                                    Claim 7; Fig 2; 11pp; Japanese
                                                                                                           Heat resistant beta-1,3-glucanase gene DNA -alkali-compatible Bacillus sp.
                                                                                                                                                                                                          20-JUL-1989;
                                                                                                                                                                                                                                                                                                                                Alkalophilic;
                                                                                                                                                                                                                                                                                                                                                       Beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                        AAR11599;
                                                                                                                                                                                                                                                                                                                                                                                                                                AAR11599 standard;
Sequence
                                                                                                                                                           WPI; 1991-113290/16.
                                                                                                                                                                                                                                  20-JUL-1989;
                                                                                                                                                                                                                                                         07-MAR-1991
                                                                                                                                                                                                                                                                                  JP03053883-A.
                                                                                                                                                                                                                                                                                                          Bacillus
                                                                                                                                                                                                                                                                                                                                                                                 18-JUN-1991
                                                                                                                                                                                 (SHKJ ) SHINGIJUTSU KAIHATSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRK----FFDARGNWKWTWDDEGDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ygtveiraklpqgdwlypeillepflkkygsmnyasgvvkiacargnaelysgpndysnt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qhmpgflddsiysgtln---lfsgctss-aeacikqasgadilppivsgri-tsigfaft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VWQDEFDYFDGAKWQ-HEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLADNINPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaggitef-rdgsitsgg---vtkpw----rdsarkasvhfwrhmsdwfprwsqp---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAP-FGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDI-PPAMSARVRTFQKYSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -slivdfvkv 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dgeewarveaprdal---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWP-RSGEIDIIETIGN-----RDFKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ifeeqfdsldenvwqieqyipiyhpeypfvsyqrnnltvstadgnlhi-----naklq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGEFLGIQKMGSTMHWGPGWD-DNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFV
                                                                                                                                              AAQ11293
 261
                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                  heat resistant.
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                                                                                                                                                                                                                                  89JP-0185928
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                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                261
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                                                                                                                       derived
                                                                                                                         from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254
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Best Loca Matches Query Match

Local

Similarity

13.8%;

Score 310; Pred. No. 1

DB .6e-21; 12;

Length 261; Indels

154;

Gaps

17;

100;

Conservative

35;

Mismatches

```
ARRESULT
AARPT
AARPT
AARPT
XX AARPT
AC AARPT
XX AARPT
XX OGES
XX Beta
XX Beta
XX 19t1
XW 19t1
XW 19t1
XX Pigm
XX OGES

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                                                                                                                                                                                                   Asenjo JA,
Savva D;
                  DNA construct encoding enzyme with beta-1,3-glucanase activity useful for modifying or degrading beta-glucan contg. material a the prepn. of e.g. food colourants, flavourings and yeast extra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oerskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beta-1,3-glucanase; Cellulomonas cellulans; Bacillus subtilis; lytic enzyme; beta-glucan degradation; cell wall lysis; pigment; colorant; flavour; yeast extract; protoplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oerskovia beta-1,3-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR97362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR97362 standard;
                                                                                                                                                                                                                                                                                                                               14-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                   25-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09612013-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                             (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225
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DB; AAT29043.
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--mlvdyvrvyg 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAMOVDYIRVYK 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGT-NLAPFDQNFHF 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYG------DNFHTFWFDWSPNGLR 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----gtvh----wdan-----ghae---ygrtsgnldfsqyhtysvewepnyir
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                                                                                                                                                                                                                           Diers I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                               94DK-0001192.
                                                                                                                                                                                                                                                                                                                                                                                 95WO-DK00414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Pro_peptide 64..306 /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Sig_peptide 36..63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -vqynefyi--
                                                                                                                                                                                                                           Ferrer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nwpgspnastp-----ipaq----
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                                                                                                                                                                                                                             Halkier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DSM 10297).
                                                                                                                                                                                                                             Ä
                                                                                                                                                                                                                             Hedegaard
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                          extracts
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RESULT
AAW56275
ID AAW5
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AC AAW5
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DT 18-A
XX Alph
KW alph
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Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequence (AAT29043) isolated from an O. xanthineolytica library. Recombinant beta-1,3-glücanase can be produced on a large scale using transformed host cells, esp. Bacillus subtilis DN1885 or ToC46. Protease-free beta-1,3-glücanase can be obtd. that is useful for lysing fungal cell walls, allowing recovery of intracellular proteins. The enzyme is also useful for the prepn. of protoplasts and for the prodn. of pigments, colorants, flavours, yeast extract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLG109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A novel beta-1,3-glucanase (AAR97362) from Oerskovia xanthineolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 42-43;
 WO9811246-A2
                                                                             Key
Peptide
                                                                                                                                                                          erythrocyte;
                                                                                                                                                                                         alpha-N-acetylgalactosaminidase;
                                                                                                                                                                                                                                                                                        AAW56275;
                                                                                                                                                                                                                                                                                                                      AAW56275 standard; Protein; 422
                                                Protein
                                                                                                                            Flavobacterium
                                                                                                                                                                                                                          Flavobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                :5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----tvh-gpgysgdn--gimgtyqhpqgwsfaddfhnfgidwtpgeitwlvd--gq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qpqfgrieariqiprgqgiwsafwmvganlpdtpwptsgeidimenvgnaphevhg----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lawsdefdgaagsapnpdvwnhetgaggwanaelqnyttsrvnsal-dgq------ 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for degrading or modifying beta-glucan-contg. Its amino acid sequence was deduced from a genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                          transfusion; blood
                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -qwpgnpdattpfp--
                                                                                                                            keratolyticus
                                                                                                                                                                                                                       keratolyticus endo-beta-galactosidase (ENDO-A) protein
                                              /note= "Signal peptide"
47..422
                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.2%; Score 296; DB 17; 25.7%; Pred. No. 4.2e-20; tive 36; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -gnlvital-----qesdgsy-----tsarlttqgnv 142
                               "F. keratolyticus ENDO-A protein"
                                                                                                                                                                          typing reaction; keratan sulphate,
                                                                                                                                                                                                                                                                                                                       ₿
                                                                                                                                                                                           endo-beta-galactosidase; ENDO-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -vfdqpfflilnvaigg-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -qqmkvdyvr 299
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#888888888

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RESULT 10
AAR67915
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AC AAR679
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AC AAR679
XX
AC AAR679
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Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               endo-beta-galactosidase (designated ENDO-A) protein. The ENDO-A protein can be used in conjugation with alpha-N-acetylgalactosaminidase to remove externally and internally linked A antigen on group Al erythrocytes. The resulting erythrocytes may be transfused into individuals who would be otherwise unable to safely tolerate a transfusion of type Al blood. The ENDO-A protein can also be used to degrade keratan sulphate (e.g. in the food industry), or in blood typing
     14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Fig 2A-2B; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated endo-beta-galactosidase - from Flavobacterium keratolyticus, used particularly for de-antigenising human erythrocytes bearing Al antigen for blood transfusions.
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                                                                  AAR67915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents the Flavobacterium keratolyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goldstein J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NYBL-) NEW YORK BLOOD CENTER INC
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                                                                                                                                                                                                                               APFDQNFHFILNVAVG-GINGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNW
                                                                                                                                                                                                                                                                                                             WFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNL 301
                                                                                                                                                                                                                                                                                                                                                                         DIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nlvlr---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSFVRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLFGEGFAFTDWDQYHIVWQDEFDY---FDGAKWQHEVTATGGGN---SEFQLY-TQDGA 62
                                                                                                                                                                                                                                                                            tmiwspndirfyv---nnsl--
                                                                                                                                                                                                                                                                                                                                           dsmehvnnesv-----myhtihngsvtnang---gstasksatynttd-ynly
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                                                                                                                                                                                KWTWDDEGDNNAMQVDYIRVYK 382
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                                                                  standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
   (first entry)
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                                                                                                                                                 mqvdyvrvyk 288
                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.8%; Score 286.5; DB 19; 27.0%; Pred. No. 5.1e-19; tive 32; Mismatches 100;
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Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ81334 encodes AAR67915 a (1-3)-beta-D-glucan sensitive facto has a high affinity for the (1-3)-beta-D-glucan found in fungal cell walls. The protein is therefore useful for clinically diagnosing mycosis, and as an antifungal agent for the removal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Pages 23-32; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding
least once -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1-3)-beta-D-glucan sensitive
   240
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                                                                                                                                                                                                                                                                                                                                                                                                                        5 LVVL-CLLFGEGFA---FTDWDQYHIVWQDEFDYFDGAKWQHEV--TATGGGNSEFQLYT 58
                                                                                                                                                                                                                                                                                                                                             QDGANSFVRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCY 118 :: |: | | | | |
                                                                                                                                                                                                                                                           yt-----sarlktqfdkswkygkieakmaipsfrgvwvmfwmsgdntnyvrwpss 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1995-060996/08
                                                                                                                                                                                                                             GEIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLP----KHSDDWN
                    FFDARGNWKWTWDDEGDNNAMQVDYIRVYK 382
                                                                 kiqggvngksafrnkvfvilnmaiggn---
                                                                                                                                tngidyhiysvewnssivkwfvngn---
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                                                                                                                                                                                                                                                                                           RTGAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRS 178
                                                                                                                                                                                                                                                                                                                                                                                       lvllccvvlhvgvariccshepkwqlvwsdeftngissdwefemgnglngwgnnelgyyr 61
                                                                                                NPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRK
                                                                                                                                                                YGDNFHTFWFDWSPNGLRFFYDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYEND
                                                                                                                                                                                                                                                                                                                         l Similarity
85; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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1..19
/label- sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.3%;
21.8%;
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myidyvrvyg 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 209; DB 16;
; Pred. No. 2.2e-11;
49; Mismatches 106
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Length 673; Indels 150;

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RESULT 11
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Best Local :
                                                                                                                                                                                                                                                                                    AAR67917-R67919 are active fragments of AAR67915, a (1-3)-beta-D-glucan sensitive factor, they have a high affinity for the (1-3)-beta-D glucan found in fungal cell walls. The proteins are therefore useful for clinically diagnosing mycosis, and as antifungal agents for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (1-3)-beta-D-glucan sensitive factor glucanase domain antifungal agent; mycosis diagnosis.
                                                                                                                                                                                                                                                                                                                                                         DNA encoding a polypeptide comprising a tetrapeptide motif least once - which may be used as an antibacterial and
                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9501432-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Limulus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR67918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR67918 standard; Protein;
                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                Claim 5; Page 40; 51pp; Japanese
                                                                                                                                                                                                                                                                                                                                                  antifungal.
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-060996/08
                                                                                                                                                                                                                                                                                                                                                                                                     Iwanaga
                                                                                                                                                                                                                                                                                                                                                                                                                     (SEGK )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (1-3)-beta-D-glucan
                                                                                                                         141
203
                 315 AVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQ 374
                                                                      128
                                                                                        201
                                                                                                        76
                                                                                                                                            53
                                                                                                                                                            81
                                                                                                                                                                                        GIQKMGSTMHWGPGWDDNRYWLTSLP----KHSDDWN-YGDNFHTFWFDWSPNGLRFFV
                                                                                                                  SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEEL 200
                                                                                                                                                                           aiggn---
                                                    DDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNV 314
                                                                    ---kvrgtihw-----stpdgahahhnresntngidyhiysvewnssivkwfv
                                                                                                       swkygkleakmaipsfrgvwvmfwmsgdntnyvrwpssgeidfie-----hrntnne--
                                                                                                                                          ------sarlktqfdk
                                                                                                                                                            NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
                                                                                                                                                                                                                Similarity
79; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                      SEIKAGAKU KOGYO CO LTD.
                                                                                                                                                                                                                                                            233 AA;
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                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                        9.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                     Oda T, Seki N;
                                                                                                                                                                                                                45;
                                                                                                                                                                                                               Score 208; DB 16;
Pred. No. 6.7e-12;
15; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233
-wpgfdvadea----fpak-----
                                  -----qyfevkiqggvngksafrnkvfvilnm
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                                                                                                                                                                                                                                 Length 233;
                                                                                                                                                                                                                Indels 146;
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                                                                                                                                                                     Query Match
Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1999
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                          09-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                           09-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                              JP10337184-A
                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW92310;
                                           147
                                                                                                                                                                                                                                                                                      glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
          198
                                                              137
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This sequence represents a novel Streptomyces sp. SGTase protein has beta-1,3-glucanase activity. A large amount of SGTase can be prepared using the recombinant DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 7-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-113611/10.
N-PSDB; AAX01742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DNIN ) DAINIPPON INK & CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGTase; beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW92310 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                       1 MRWTLVVL--CLLEGEGEAFT-------DWDQYHIVWQDEED-----YEDGA 38
EFLGIOKMGSTMHWG---PGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNG----
                                                             --veariqvpnvtgdaakgywpafwmlgapyrgdywnwpavgeldime-----
                                                                                                          VVVHAKMPV----GD---WLWPAIWML--PEDWYYGGWPRSGEIDIIETIGNRDFKNTGG 197
                                                                                                                                                                                               GTDFMYNGVLDVWAMYGACTNTDNNGCYRTG----AAGDIPPAMSARVRTFQKYSFTHGR 146
                                                                                                                                                                                                                                       dwry-atgtgypggpsnwgtgeietmtsnpenvsldgngnlritp----- 136
                                                                                                                                                                                                                                                                                   KWQHEVTATG-----GGNSEFQLYTQDGAN-SFVRDGKLFIKPTLLADNINPQTGAPF 90
                                                                                                                                                                                                                                                                                                                         lrrtlvalagalalgag-altltgptasasvppppsgwtg---vfaddfdgpkgsgvdtg 92
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp. SGTase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97JP-0151321.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         7.5%;
24.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 168.5; DB 2
Pred. No. 6.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       108; Indels 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
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f
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                                                                                                                              Query Match
Best Local S
Matches 80
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                                                                                                                                                                                                                        The present invention relates to Mycobacterium tuberculosis secreted proteins (MTSP), where the polypeptide has M. tuberculosis specific antigenic and immunogenic properties. Compositions of the invention representation of the protein for diagnosing Mycobacterium tuberculosis infection and as
                                                                                                                                                                                                                                                                                 Claim 11;
                                                                                                                                                                                                                                                                                                                                                                             Gennaro ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB52463;
                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                            Novel Mycobacterium tuberculosis secreted polypeptides and polynucleotides useful in diagnosis, treatment and prophyl tuberculosis
                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-007151/01
                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAY-1999;
04-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                    (PUBL-) PUBLIC HEALTH RES INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200066143-A1
                                                                                                                                                                                                              vaccine against M.
             135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 --qgmntvfatmhcgtspggpcnetsg1ggqttcqgttcqagfhtyrmewdrssdveeir
                                                                                                                                          Local Similarity
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                                                                                                        26
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            RTFOKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWP-RSGEIDIIETIGNRDFK 193
                                                                             llfhdefdgpagsvpdpskwqvsnhrtpiknpvgfdrpqffgqyrdsrqnvfldg-----
                                                                                                       IVWQDEFD-----YFDGAKWQ---HEV---TATGGGNSEFQLYTQDGANSFVRDGKLFIK 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | .| ::| |||::|
-dagtqpghsmlvdyvqv 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dhgffvilnvamgg--gf-pdaf---
                                                         PTILLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDEG--DNNAMQVDYIRV 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTW
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                                                                                                                                                                                                                                                                                Fig 1;
                                                                                                                                                                                          294 AA;
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                             Gomez MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                          990S-0132479.
990S-0132503.
                                                                                                                                                                                                                                                                               60pp;
                                                                                                                                                                                                              tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                         6.2%;
                                                                                                                                                                                                                                                                                English.
                                                                                                                              43; Mismatches
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                                                                                                                                         Score 138.5; DB:
Pred. No. 3.6e-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; MTSP; vaccine
                                  ----hg1wr---
                                                                                                                                                    DB 22;
                                                                                                                              102;
Indels
                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                 prophylaxis
                                  -ggigttweari
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                                                                                                                                                     294;
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RESULT 1
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                                                                This polypeptide is immunologically reactive with antibodies raised against a pure endo-1,3(4)-beta-glucanase from T. harzianum CBS 243.71. Using this sequence, the protein may be expressed recombinantly in transformed host cells, particularly Aspergillus oryzae or Aspergillus niger. Typical applications of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast; fungus; enzyme; endo-beta-glucanase; EC-3.2.1.6; hydrolase; endo-1,3(4)-beta-glucanase; beta-glucan degradation; hydrolysis; detergent; surfactant; fungicide; antifungal; cleaning.
                                                                                                                                                 Claim 1; Page 40; 57pp; English.
                                                                                                                                                                              DNA encoding endo-beta-glucanase from Trichoderma harzianum useful, e.g., in food processing, as antifungal agent, in cl compsns., etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trichoderma
Sequence
                         recombinantly produced protein are preparation of and yeast extracts, brewing, wine and press-juice foods and feeds, as antifungal agents, etc.
                                                                                                                                                                                                                                    WPI; 1996-010920/01.
N-PSDB; AAT09876.
                                                                                                                                                                                                                                                                         Kauppinen
                                                                                                                                                                                                                                                                           Andersen LN,
Kauppinen MS,
                                                                                                                                                                                                                                                                                                                   (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                         11-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                               WO9531533-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trichoderma harzianum CBS 243.71.
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Kofod LV, Olsen
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Query Match Best Local S Matches 86

Similarity

5.9%;

Pred. No. 0.00017;

Conservative

40;

Mismatches

109;

Length Indels

292; 151;

Gaps

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            The present sequence represents the filamentous fungus Phaffia rhodozyma (CBS No. 6938) endo-1,3(4) beta glucanase sequence. The enzyme may be used for modification or degradation of material which contains beta-glucan. Therefore the enzyme is claimed to be useful in, e.g. brewing, wine-making, preparation of protoplasts from yeasts, or preparation of pigments, colourants or flavourants. The enzyme is also claimed to be useful in the preparation of
                                                                                                                                  Claim 2; Pages 27-28; 36pp; English.
                                                                                                                                                               Enzyme with endo-1,3(4)-beta-glucanase activity - which is useful in, e.g. brewing, wine-making, preparation of protoplasts from yeasts, or preparation of pigments, colourants or flavourants
                                                                                                                                                                                                                                WPI; 1998-506310/43.
N-PSDB; AAV59143.
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pharmaceuticals.
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Search completed: October 11, 2001, 15:51:39
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Perfect score:
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-712-072C-4
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US-08-712-072C-2
US-09-330-945-2
US-09-330-945-2
US-09-286-690-10
US-09-286-690-7
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US-09-110-295-21
US-09-110-295-21
US-09-120-365-5
US-09-120-365-5
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US-08-712-072C-3
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US-08-508-761B-34	US-08-867-484A-2	US-09-262-653A-4	US-08-580-545B-4	US-08-941-445A-15	US-08-812-829-6	US-08-814-052-6	US-09-390-200-2	US-08-749-391-2	US-08-451-409A-1	US-09-286-690-8	US-09-124-541-1	US-08-928-692-17	US-08-956-268-5	US-08-797-366-5	US-09-255-502-7	US-08-941-445A-17	5457037-5
Sequence 34, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 15, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 8, Appli	Sequence 1, Appli	Sequence 17, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 7, Appli	Sequence 17, Appl	Patent No. 5457037

ALIGNMENTS

Sequence 3, Application US/08712072C Patent No. 5925541 REFERENCE/DOCKET NUMBER: 63475/97 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 697-5995 TELEFAX: (212) 286-0854 or 286-0082 TELEX: TWX 710-581-4766 INFORMATION FOR EQ ID NO: 3: SEQUENCE CHARACTERISTICS: GENERAL INFORMATION: HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE: MOLECULE TYPE: ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: US/08/712,072C FILING DATE: 11-SEP-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE COMPUTER: IBM PC COMPATIBLE COMPATEM: MS-DOS SOFTWARE: ASCII CURRENT APPLICATION DATA: TITLE OF INVENTION: ENUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS STREET: 90 Park CITY: New York STATE: NY NAME: Bogosian, Elizabeth A REGISTRATION NUMBER: 39,911 COUNTRY: TOPOLOGY: STRANDEDNESS: ADDRESSEE: LENGTH: 321 amino acids 10016 amino acid E: Amster, Rothstein & Ebenstein 90 Park Avenue Jack Goldstein, Alex Zhu and Lin SD e13b, linear peptide Bacillus circulars ENDO-BETA-GALACTOSIDASE 13 Leng

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                                                ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A
REGISTRATION UNMBER: 32,503
REFERENCE/DOCKET NUMBER: FUN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                   TELEFAX: (617) 248-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL POLYPEPTIDE AND DNA ENCODING TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                          CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MUTA, TATSUSHI
APPLICANT: SEKI, NORIAKI
APPLICANT: ODA, TOSHIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 -- AMNDSKSPQDP-----SGKI 145
                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 28-FEI CLASSIFICATION: 53/
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                                                                                                                                                                                                                                                                                                                 ZIP: 02109
                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ
ADDRESSEE: THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KWTWDDEGDNNAMQVDYIRVYK 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFDEPFYLIMNLAVGGNFDGGRTP----NASDIPA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLIWQDEFNETTLDTSKWNYFTGYYLNNDPATWGWGNAELQHYTNSTQNVYVQDGKLNIK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFDQNFHFILNVAVGGT--NGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNW 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SG-----TIHFGGQWPVNQ-----SSGGDYHFPEGQTFANDYHVYSVVWEED 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   BOSTON
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                                   (617)
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                                                                                                                                                                   UMBER: US/08/392,828C
28-FEB-1995
                                  248-7100
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26.2%;
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                   37:
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                                                                                        FJN-033
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Pred. No. 2.8e-28;
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                                                                                                                                                                                                                              Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: FEATURE:
                                                                  SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR,
ADDRESSEE: THIBEAULT, LLP
                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB
TITLE OF INVENTION: AMEBOCYTE LYSATE FACTOR G SUBUNIT
NUMBER OF SEQUENCES: 39
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 TGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWN-----YGDNFHTFWFDWSPN 248
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                                                                                                                                                                                                                               STREET: 125 I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 NTKDKLSLKYGRVDFRAKLPTGDGVWPALWMLPKDSVYGTWAASGEIDVMEARGRLPGSV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 A-----MNDSKSFPQDP-----NRYAQYS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein LOCATION: 1..262 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
                                 FILING DATE:
                                                  APPLICATION NUMBER:
                                                                                                                                                                            COUNTRY: U:
ZIP: 02110
                                                                                                                                                                                                                STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KWTWDDEGDNNAMQVDYIRVYK 382
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                                                                                                                                                                                                                                                   125 HIGH STREET
                                                                                                                                                                                             USA
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SEKI, NORIAKI
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                                                                                     PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -IMQVDYVRVYK 260
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                                                                                                                                                                                                                                                                                                                                                                            TOSHIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "BG1 A1 SEQUENCE (FIGURE 2)
                                                                                       Release #1.0,
                                                    US/09/330,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -NASDIPA--
                                                                                       Version
                                                                                                                                                                                                                                                                                    TESTA, HURWITZ
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COMPUTER:

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LOCATION: 1..262
OTHER INFORMATION: /note- "BG1 A1 SEQUENCE (FIGURE --09-330-945-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                              Sequence 4, Application US/08712072C Patent No. 5925541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                     TITLE OF INVENTION: ENDO-BETA-GALACTOSIDASE YORBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                WERAL INFORMATION:
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                            COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 27, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/119,995 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                STATE:
                                                                                   CITY: New York
                                                                                               STREET:
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: PITCHER, EDMUND
                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 NLIWQDEFNGTTLDTSKWNYETGYYLNNDPATWGWGNAELQHYTNSTQNVYVQDGKLNIK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NTKDKLSLKYGRVDFRAKLPTGDGVWPALWMLPKDSVYGTWAASGEIDVMEARGRLPGSV 146
                                                                                                                                                                                                                                                                                                                                  KWTWDDEGDNNAMQVDYIRVYK 382
                                                                                                                                                                                                                                                                                                                                                                                  PFDEPFYLIMNLAVGGNFDGGRTP----NASDIPA
                                                                                                                                                                                                                                                                                                                                                                                                               PFDQNFHFILNVAVGGT--NGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNW 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLRFFVDDE-----NQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWN-----YGDNFHTFWFDWSPN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A-----NNDSKSFPQDP-----NRYAQYS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARV 134
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                                                                                            E: Amster, Rothstein & Ebenstein
90 Park Avenue
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26.2%;
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Pred. No. 7.6e-28;
4; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----SSGGDYHFPEGQTFANDYHVYSVVWEED 188
                                                                                                                                                                                                                                                                                                                                                                                                                                               -----QWYSTAAPNNPN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
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                 Sequence 2, Applicating Patent No. 5919688
GENERAL INFORMATION:
APPLICANT: Ferrer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: TWX 710-581-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                 258
                                                                                                                                                                                                                                                                                                               183
                                                                                                                                                                                                   335 ALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIRVYK 382
                                                                                                                                                                                                                                                                         275 WYDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDP 334
                                                                                                                                                                                                                                                                                                                                                                                                                        170 WVYGG--WPRSGEIDIIETIG-NRD-----FKNTGGEFLGIQKMGSTMHWGPGWDDNRY 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 TNTDNNGCYRTGAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPED 169
                                                                                                                                                                                                                                                                                                                                                221 WLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDE-----NQALLDVPYPLIDANPW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 11-SEP-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bogosian, Elizabeth REGISTRATION NUMBER: 39,91 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
SOFTWARE: ASCII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRWTLVVLCLLFGEGFAFTD-----WDQYHIVWQDEFDYF---DGAKWQHEVTATGGG
                                                                                                                                                                                                                                                                                                               --IRVPTARTD----FHVYAIEWTPEEIRWFVDDSLYYRFPNERLTD---PEADWRHW
                                                                                                                                                                                                                                                                                                                                                                                      QTYGSAYWPDNGEIDIMEHVGFNPDVVHGTVHTKAYNHLLGTQRGGS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NQELQYYTRARIENARVGGGVLIIEA----RHEPYEGREY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSEFOLYTODG-ANSFVRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGAC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRRTAFLLSVLIGCSMLGSDRSDKAPHWE----LVWSDEFDYSGLPDPEKWDYDVGGHGWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                        Application US/08824707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 286-0854 or 286-0082
FWX 710-581-4766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 amino acids
Ferrer, Pau
Diers, Ivan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gub, Rhodothermus marinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.4%; Score 344.5; DB 2; 27.5%; Pred. No. 4.2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MS-DOS
                                                                                                                                                               -EAFPAQ----
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                                                                                                                                                                                                                                       -PFDQPFHLIMNIAVGGAWGG----
                                                                                                                                                                 -LVVDYVRVYR 273
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APPLICANT:

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RESULT 6
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Best Local (
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NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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LENGTH: 306 amino acid
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MEDIUM TYPE: Floppy disk
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
                                                                                                              380 VY 381
                                                                                                                                                                                                                                                                                                            199 -----TVH-GPGYSGDN--GIMGTYQHPQGWSFADDFHTFGIDWTPGEITWLVD--GQ 246
                                                                                                                                                                                                                                                                                                                                                                                         143 QPQFGRIEARIQIPRGQGIWSAFWMVGANLPDTPWPTSGEIDIMENVGNAPHEVHG---- 198
                                                                                                                                                                                                                                                                                                                                                                                                                           141 SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL 200
                                                                        300 VY 301
                                                                                                                                                                                           320 NGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIR 379
                                                                                                                                                                                                                                                                        260 ALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGT 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 IVWQDEFDYFDGAK-----WQHEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLAD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/824,707 FILING DATE: 14-April-1997 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                  GIQKMGSTMHWGPGWD-DNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQ 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAWSDEFDGAAGSAPNPDVWNHETGAGGWGNAELQNYTTSRVNSAL-DGQ------ 116
                                                                                                                                                                                                                                   EYHRVTTADVGANQW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: No. 59196880 No. 5919688disk of No. 5919688th America, 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 amino acids
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Cavva, Demitris
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                                                                                                                                                       QWPGNPDATTPFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.7%; Score 307; DB 2; Length 306; 26.2%; Pred. No. 3.1e-23; ative 36; Mismatches 97; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. 5919688el enzyme with beta-1,3-glucanase activity
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                                                                                                                                                       -QQMKVDYVR 299
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Best Local Similarity 27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08712072C Patent No. 5925541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 286-0854 or 286-0082 TELEX: TWX 710-581-4766 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 285 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 11-SEP-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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APPLICANT: Jack Gold
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
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CITY: New York
STATE: NY
                                                                                                                   136 DSMEHVNNESV------MYHTIHNGSVTNANG---GSTASKSATYNTTD-YNLY 179
                                                                                                                                                                                                                          123 AGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPED-WVYGGWPRSGEI 181
302 APFDQNFHFILNVAVG-GTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNW 360
                                                                                                                                                         182 DIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTF 241
                                                                            242 WFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNL 301
                                                                                                                                                                                               76
                                                                                                                                                                                                                                                                          65 NLVLR-----
                                                                                                                                                                                                                                                                                                                  63 NSFVRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGA 122
                                                                                                                                                                                                                                                                                                                                                                                         10 LLFGEGFAFTDWDQYHIVWQDEFDY---FDGAKWQHEVTATGGGN---SEFQLY-TQDGA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bogosian, Elizabeth REGISTRATION NUMBER: 39,91 REFERENCE/DOCKET NUMBER: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                               AGDPVAYHAGGVKSMGKFSMTYGKVEVRAKFTQGRGSWPAIWMMPEPATAYGGWPSCGEI 135
                                                                                                                                                                                                                                                                                                                                                       LLNATTVATTD---YELIWSDEFNSSGGFDSTKWSYADRGTVAWNKYMTSLPAYASQDGS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Amster, Rothstein & Ebenstein 90 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285 amino acids
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VENTION: ENDO-BETA-GALACTOSIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No. 3.
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                                    QYTYARVSGGGTQQ 210
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MOLECULE TYPE: pe
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRACMENT TYPE: N-
; ORIGINAL SOURCE:
US-08-712-072C-2
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                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                            Matches 105;
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TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 697-5995
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NAME: Bogosian, Elizabeth A.
REGISTRATION NUMBER: 39,911
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PRIOR APPLICATION DATA:
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 109
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                                                                                                67
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                                                                                                                                                           10 LLFGEGFAFTDWDQYHIVWQDEFDY---FDGAKWQHEVTATGGGNSEFQLYTQDGANSFV 66
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TOPOLOGY: li
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                              PPAMSARVRTFQKYSFTHGRVVVHAK-----MPV---GDWLWPAIWMLPED-WVYGGWPR 177
                                                                                            RDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDI 126
                                                                                                                            LLNATTVATTD---YELIWSDEFNSSGGFDSTKWSYADRGTVAWNK--YMTSQDGSNLVL 99
PVAYHAGGVKSMKFSMTYGKVEVRAKFTGVSLPAYAQGRGSWPAIWMMPEPATAYGGWPS
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DN: ENDO-BETA-GALACTOSIDASE
                                                                                                                                                                                                                                                                                                                                                                                        single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286-0854 or 286-0082
                                                                                                                                                                                           12.2%; Score 272.5; DB 2 27.2%; Pred. No. 1.6e-19; Live 29; Mismatches 97
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                                                                                                                                                                                                                         Length 422;
                                                                                                                                                                                            Indels 155;
                                                                                                                                                                                         Gaps
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                                                                                                                                     Query Match
Best Local S
Matches 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 654 amino acids
                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL POLYPEPTIDE AND DNA ENCODING
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56
                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
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ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                   23 QYHIVWQDEFDYFDGAKWQHEV--TATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLAD 80
                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
                                                                  KWQLVWSDEFTNGISSDWEFEMGNGLNGWGNNELQYYRRE--NAQVEGGKLVI----- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGNWKWTWDDEGDNNAMQVDYIRVYK 382
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                                                                                                                                 ch 9.3%; Score 208; DB 1; Length 654; I Similarity 21.5%; Pred. No. 1e-12; 79; Conservative 45; Mismatches 98; Indels 1
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SEKI, NORIAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IWANAGA, SADAAKI
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-TAKREDYDGFKYT----
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                                                                                                                                       Indels 146;
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-SARLKTQFDK 78
                                                                                                                                       Gaps
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                                                                          ; MOLECULE TYPE: protein US-09-330-945-2
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 Query Match
Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB
TITLE OF INVENTION: AMEBOCYTE LYSATE FACTOR G SUBI
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ
ADDRESSEE: THIBEAULT, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R
                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 654 amino acid
                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 NGN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 DDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNV 314
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79
                                                                                                        TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 5JI
                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: BOSTON
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5, 6077946
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                                                                                                                                    654 amino acids
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MUTA, TATSUSHI
SEKI, NORIAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ODA, TOSHIO
                                                                                                                                                                                     (617)
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version
                                                                                                                                                                                                  (617)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                 7) 248-7100
248-7100
200: 2:
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   45;
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Score 208; DB 3; Length 654;
Pred. No. 1e-12;
5; Mismatches 98; Indels 1
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   Indels 146;
   Gaps
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TOPOLOGY: US-08-737-526-4
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Patent No. 5871966
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APPLICANT: Kofod, Lene Venke
                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Andersen, Markus Sakarı
APPLICANT: Kauppinen, Markus Sakarı
APPLICANT: Christgau, Stephan
APPLICANT: Christgau, Stephan
TITLE OF INVENTION: An Enzyme With Endo-1,3(4)-B-Glucanase
                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,526
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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227 IDYVRVYQ 234
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                                                  LENGTH:
TYPE: a
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                                                                                                                        TELEPHONE: 212-00.
TELEPHONE: 212-878-9655
                                                                                                                                                                                           NAME: Valeta, Gregg A
REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM CON OPERATING SYSTEM: SOFTWARE: FastSE(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81
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                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQ 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---KVRGTIHW-----STPDGAHAHHNRESNTNGIDYHIYSVEWNSSIVKWFV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWKYGKIEAKMAIPSFRGVWVMFWMSGDNTNYVRWPSSGEIDFIE-----HRNTNNE-- 130
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                                                amino acid
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                                                                 292 amino acids
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                linear
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                                                                                                                                                                                               4174.204-US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5871966th America, Inc.
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US-09-098-580-4
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09098580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                            APPLICATION NUMBER: 08/7:
FILING DATE: 08-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61400960 No. 6140096d1sk of
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: An Enzyme With Endo-1,3(4)-B-Glucanase TITLE OF INVENTION: Activity
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              TELECOMMUNICATION INFORMATION:
                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                              REFERENCE/DOCKET NUMBER:
                                              NAME: Valeta, Gregg A REGISTRATION NUMBER:
                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARGNWKWTWDDEGDNNAMQVDYIRVY 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---NNIA--HSPLFFILNVAVGG-----NWPGNP--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYTFTPAAGKVTRLEAAIRFGSNAQANKQGIWPAFWMLGDSLRQPGGSWPNCGEIDIMET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --QLVPWRDSSKGT-----STFGGWT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADNINPQTGAPEGTDEMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FNLVWTDTFAGNGGTSPNQNNW-NIITGNLNVNAEQETYSSSTANVQLSGGS-----TL-
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                                                                                                                                                                                                                                                                                                                                                                         405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kauppinen, Markus Sakari
Christgau, Stephan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andersen, Lene No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kofod, Lene Venke
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212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DGYGSMMEVGYVAQY 290
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22.0%; Pred. No. 3.1
                                                                                                                 08/737,526
                   35,127
RER: 4174.204-US
                                                                                                                                                                                       US/09/098,580
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Applic Patent No. 5344777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
COMPUTER: IBM PC compat
OPERATING SYSTEM: MS DO
SOFTWARE: ASCII FORM
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
                                                                                                                                                                                                                                            APPLICANT: Kawamura, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.72
COMPUTER: IBM PC compatible
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARGNWKWTWDDEGDNNAMQVDYIRVY 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V---DGQATGHGTLHCDYYPGGICNEGNGI-GGPVNIANVNDWHAWRVEIDRTPSSW---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---NNIA--HSPLFFILNVAVGG--
                                                                                                                 10016-2088
                                                                                                                                                                New York
                                                                                                                                                                                                                                                                             r: Okumura, Hajime and
I: Kawamura, Yoshiya
INVENTION: Structural Gene of Membrane-Bound
INVENTION: Alcohol Dehydrogenase Complex, Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/07985458
                                                                                                                                                New York
                                                                                                                                                                                 600 Third Avenue
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Fukaya, Masahiro;
                                                                                                                                                                                                                                                                                                                                                                           Takemura, Hiroshi;
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                                                MS DOS
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     US/07/985,458
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                                                                 (NEC PC-9801 ES)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 17081
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)972-1400
                 205
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                                              379 AKTGEFI-----SGKNYVYVNWASGLDPKTG-----RPIYNPDALYTLTGKEWYGIPGD 427
                                                                                                               319
                                                                                                                                                                             259 KAYQTWSPTGAWTRQGGGGTVWDSIVYDPVADLVYLGVGNGSPWNYKYRSEGKGDNLFLG 318
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CLASSIFICATION: 435
RIOR APPLICATION DATA:
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FILING DATE: 20-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fitle:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 73440/1990 FILING DATE: 26-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COPOLOGY:
MG----STMHWGPGWDDNRYWLTSLP-----
                                                                               MPVGDWLWPAIWMLPEDWVYGGW-----PRSGEIDIIETIGNRD--FKNTGGEFLGIQ-K 204
                                                                                                            SIVALKPETGEYVWHFQETPMDQWDFTSDQQIMTLDLPINGETRHVIVHARKNGFFYIID 378
                                                                                                                                              ---- IPPAMSARVRTFQ----- KYSFTHGR----
                                                                                                                                                                                                              GVLDVWAMYGACTNTDNNGC----
                                                                                                                                                                                                                                                GNGGSEF------GARGFVSAFDAETGKVDWRFFTVP-----NPKNEPDAASDSVLMN 258
                                                                                                                                                                                                                                                                               GGGNSEFQLYTQDGANSFVR-----
                                                                                                                                                                                                                                                                                                                                                                                                                  1991
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polyoxogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cloning and Sequencing of the Gene Cluster
Encoding Two Subunits of Membrane-Bound
Alcohol Dehydrogenase from Acetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                  292-300
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Kawamura, Yoshiya;
Nishiyama, Makoto;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tamaki, Toshimi;
Fukaya, Masahiro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (212)370-1622
                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acetobacter altoacetigenes
                                                                                                                                                                                                                                                                                                              5.0%; Score 112.5; DB 1; 20.4%; Pred. No. 0.0062; Live 37; Mismatches 113;
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               ----KHSDDWNYGDNFHTFWFD
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; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-286-690-10
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US-09-286-690-7
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Best Local Similarity 21.9%;
Matches 60; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 10
                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                               Sequence 7, Application US/09286690 Patent No. 6103511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10,
                                    APPLICANT: Li, Xin-Liang
APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
TITLE OF INVENTION: Lichenase and Coding Sequences
FILE REFERENCE: 55-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Li, Xin-Liang APPLICANT: Ljungdahl, Lar APPLICANT: Chen, Huizhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
CURRENT APPLICATION NUMBER: US/09/286,690 CURRENT FILING DATE: 1999-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1997-10-03 NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/286,690 CURRENT FILING DATE: 1999-04-05 EARLIER APPLICATION NUMBER: US 60/027,882 EARLIER FILING DATE: 1999-10-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               428
                                                                                                                                                                                                                                                                                                                                                                           160 EKIYNLGFDAANSYHTYAFDWQPNSIKWYVDGQLKHTATTQIPQTPGKIMMNLWNGAGVD
                                                                                                                                                                                                                                                                                                                                                                                                                    229
                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 TG-PTDGTPWDEIDI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 GGWPRSG----EIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKH 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 MSARVR-----TFQKY-----SFTHGRVVVHAKMPVGDWLWPA--IWMLPEDWVY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          526 TGGDLLFQGLANGEFHAYDATNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 APEDQUEHFILN --- VAVGGTNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 LFIKPTLLADNINPQTGAPFGTDF-MYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPA 129
                                                                                                                                                                                                                                                                                                                                                                                                                    SDDWNYG----DNFHTFWFDWSPNGLRFFVDDE---NQALLDVPYP--LIDANPW---WVD
                                                                                                                                                                                                                                                                                                                                  FWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFI 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFLSLSTFAASASAQTGGSFYEPFNNYN--TGLWQKADGYSNGNMFNC--TWRANNVSMT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1999-10-04
APPLICATION NUMBER: PCT/US97/17811
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                                                                                                                                                                                                                                                                                         -NGVTPLSRSLHWV 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
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Pred. No. 0.0023;
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EARLIER APPLICATION NUMBER: US 60/027,882 EARLIER FILING DATE: 1999-10-04

APPLICATION NUMBER: PCT/US97/17811

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Best Local 9
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LENGTH: 238
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SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                 CLASSIFICATION: 473.
PRIOR APPLICATION UDATA:
APPLICATION UDABER: US 07/773,652
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Von Wettstein, Dietrich
TITLE OF INVENTION: A Thermostable (1,3-1,4)-beta-Glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 KHTATTNIP----STPGKIMMNLWNGTGVDSWLGSYNGANP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 QKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYG----DNFHTFWFDWSPNGLRFFVDD-- 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watch 4.7%;
Local Similarity 22.0%;
                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                  CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 HIVWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQDGAN-SFVRDGKLFIKPTLLADNIN 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENQALLDVPYPLIDANPWWVDFWEWG----KPWLPQYENDNP 294
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Hofemeister, Jurgen
Thomsen, Karl Kristian
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   NUMBER:
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                                                                                                                                                                  US/08/103,998
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30307/123
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Pred. No. 0.0056;
                                                                                                                                                                                                      Version #1.25
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
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TELEFHONE: (703) 836-9300
TELEFAX: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                 275 WYDFWEWG----KPWLPQYENDNP 294
                                                                        146 YTNGAGNHEKFADLGFDAANAYHTYAFDWQPNSIKWYVDGQLKHTATTQIP---
                                                                                                                                                                              207 --- STMHWGPGWDD------NRYWLTSLPKHSDDW---
                                                                                                                                                                                                                                                   156 GDWLW-PAIWMLPEDWVYG-GWPRSGEIDIIETIGNRDFKNTGGEFLGIQKMG----- 206
201 KIMMNLWNGTGVDDWLGSYNGVNP 224
                                                                                                                                                                                                                                                                                                   Local Similarity 20.6%;
                                                                                                                                           86 EYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGPAHGTQWDEIDIEFLGKDTTKVQFNY 145
                                                                                                                                                                                                                  26 GSVFWEPLSYFNPSTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKLGLTSSAYNKFDCA 85
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                               237 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                        -FHTFWFDWSPNGLRFFVDDE---NQALLDVPYPLIDANPW 274
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Pred. No. 0.023;
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                                                                        -- AAPG 200
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Search completed: October 11, 2001, 15:52:05 Job time: 208 sec

GenCore version Copyright (c) 1993 - 2000

4.5 Compugen Ltd

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Title:
Perfect score:
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Maximum Match 100%
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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probable beta-gluc
KRE6 protein - yea
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                                                                                                                                                                                         hypothetical prote
Avicelase III - As
Licheninase (EC 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable secreted
probable beta-1,3-
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probable glucanase
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hypothetical prote
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endo-1,4-beta-xyla
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glucan endo-1,3-be
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licheninase (EC 3.
Gram-negative bact
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      GGVNYF---
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ALIGNMENTS

beta 1,3-glucanase (EC 3.2.1.-) precursor - sea urchin (Strongylocentrotus purpuratus C;Species: Strongylocentrotus purpuratus (purple urchin) C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 21-Jul-2000 C;Accession: JC6141; PC6037 C;Accession: JC6141; PC6037 R;Bachman, E.S.; McClay, D.R.
Proc. Natl. Acad. Sci. U.S.A. 93, 6808-6813, 1996
A;Title: Molecular cloning of the first metazoan beta-1,3 glucanase from eggs of the efense enzymes in plants.
efense enzymes in plants.
eff: egg; glycosidase; hydrolase
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-499/Product: beta 1,3-glucanase #status predicted A;Molecule type: protein
A;Residues: 21-40;197-209;329-344 <BA2>
A;Experimental source: egg
C;Comment: This enzyme functions in several extracellular activities including autoca A; Molecule type: mRNA A; Residues: 1-499 <BAC> A; Cross-references: GB:U49711; NID:g1488256; PIDN:AAC47235.1; A;Reference number: JC6141; MUID:96270625 A;Accession: JC6141 A; Accession: PC6037 Query Match Best Local 179 LIFQEEFDSFNLDIWEHEMTAGGGGNWEFEYYTNNRSNSYVRDGKLFIKPTLTTDKL--- 235 Local Similarity KYGRLEVEAKLPTGDWLWPAIWLLPKHNGYGEWPASGEIDLVESRGNADIKDADGLSAGV GGTNGFIPDGCINRGGD-----PALOKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNN 371 ----LLLNVDP-ATGFWDLG-----EFENDAPGIDNPWAYNPNKLTPFDQEFYLILNVAV DVPYPLIDANPWWVDFWEWGKFWLPQYEN-----DNPWAGGTN-LAPFDQNFHFILNVAV 316 DQMGSTMHWGPFWPLNGY----PK--------GEGSLSSGTLDLWGSSPANLCTGNAWYGCSRTGSNDNLLNPIQSARLRTVESFSF 290 TGAPFGTDFMYNGVLDVWAMYGA--CTNTDNNGCYRTGAAGD-IPPAMSARVRTFQKYSF 142 158; Conservative -----GDGLTYTPA--KPWSNDS--PTASKDFWSDFNTWYPTWN--GEEA 476 31.8%; 42.7%; 48; Score 713; DB 2; Pred. No. 4.7e-50; Mismatches 88; Length 499; --THATKFYVDDE----Indels <MAT> PID:g1488257 Gaps 431 381 350 15;

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) 문
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A;Accession: PN0613
A;Molecule type: protein
A;Residues: 39-58 <YA2>
                                                                                                                                 RESULT
T18265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;1-38/Domain: signal sequence #status predicted <SIG> F;39-877/Product: glucan endo-1,3-beta-D-glucosidase #status predicted
                                     C; Accession: T1
R; Schwarz, W.H.
                                                                      endo-1,3(4)-beta-glucanase (EC 3.2.1.6) - Clostridium thermocellum
C;Species: Clostridium thermocellum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Yanamoto, M.; Aono, R.; Horikoshi, K.
Bioscl. Biotechnol. Blochem. 57, 1518-
A;Title: Structure of the 87-kDa beta-1
A;Reference number: JN0772; MUID:940338
A;Accession: JN0772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) precursor N;Alternate names: beta-1,3-glucanase C;Species: Bacillus circulans C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_chC;Accession: JN0772; PN0613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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submitted to the EMBL Data Library, July 1995 A; Reference number: 218848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                             DDEGDNNAMQVDYIRVYK 382
                                                                                                                                                                                                                                                                                                    NFHFILNVAVGGT--NGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTW 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFV 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTKDHFSLKYGRVDFRAKLPTGNGIWPALWMLPQDNVYGTWASSGEIDVMEAKGRLPGST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLIWQDEFNGTALDQSKWNYETGYYLNDDPNTWGWGNSELQHYTDRAQNVFVQDGKLNIK 486
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7-kDa beta-1,3-glucanase
MUID:94033858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----AQYS-----
                                                                                                                                                                                                                                                                                                                                                               -GKFFFKVTRDQWYSAAAPNNP
                                                                        #text_change 15-Oct-1999
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A; Accession: T18265
A; Status: preliminary; translated
A; Molecule type: DNA
A; Residues: 1-1324 <SCH>
A; Cross-references: EMBL:X89732;
C; Genetics:
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C;Keywords: hydrolase;
                                                                                          A;Gene: glcA
F;1-38/Domain: signal sequence #status predicted <SIG>
F;39-682/Product: beta-1,3-glucanase Al #status predic
                                                                                                                                                                                                                          A; Accession: JQ0420
A; Molecule type: DNA
A; Residues: 1-682 < YAH>
                                                                                                                                                                                                                                                                                                                                                                         C; Species: Bacillus circulans
C; Date: 07-Sep-1990 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                              beta-1,3-glucanase Al precursor - Bacillus circulans
C;Species: Bacillus circulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                  A;Experimental source: strain WL-12
C;Comment: This enzyme, together with chitinase,
                                                                                                                                                                                                                                                                                A; Title: Structure of the gene encoding beta-1,3-glucanase Al of A; Reference number: JQ0420; MUID:90185240
                                                                                                                                                                                                                                                                                                                     R; Yahata, N.; Watanabe, T.; Nakamura, Y.; Yamamoto, Y.; Kamimiya, Gene 86, 113-117, 1990
                                                                                                                                                                                                      A;Cross-references: GB:M34503; NID:g142972; PIDN:AAA22474.1; PID:g142973
                                                                                                                                                                                                                                                                                                                                                         C; Accession: J00420
                                                                                                                                                                                                                                                                                                                                                                                                                                     JQ0420
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Best Local S
Matches 100
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                     Query Match
Best Local
                                                                                                                                                    Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YIRVYKRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGG--TNLAPFDQNFHFILNVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSWKYGKFEIRAKMPQGQGIWPAIWMMPEDEPFYGTWPKCGEIDIMELLGHEP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSFTHGRVVVHAKMPVGDWLWPAIWMLPEDW-VYGGWPRSGEIDIIETIGNRDFKNTGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---KEDITEPSGETYHYT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOYHIVWQDEFD--YFDGAKWQHEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTNGF I PDGC I NRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----DKIYGTIHFGEPHKESQGTYT-LP---EGQTFADDFHVYSIEWEPGEIRWYIDGK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQK 139
 100;
                 Similarity
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 Conservative
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                   15.7%;
26.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.8%; score 353; DB 2; 27.2%; Pred. No. 1.9e-20; ive 51; Mismatches 93;
 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NID:g1143428; PID:e190085; PIDN:CAA61884.1
Score 351.5; DB 2;
Pred. No. 1.1e-20;
4; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -YPDETTVF----
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                                                                                            predicted
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                                  Length
   Indels
                                                                                                                                                                      for hydrolyzing
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                                      682;
 149;
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                                                                                                                                                                                                                                                                                                     Bacillus circulans
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 Gaps
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424

25

241	Db 193IRVPTARTDFHYYAIEWTPEEIRWFVDDSLYYRFPNERLTDPEADWRHW Qy 275 WVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDP	6 B
192 274		S B :
169 145 220	QY 110 TNTDNNGCYRTGAAGDIPPAMSARVRTFQKYSFTHGRVVYHAKMEVGDWLWPAIWMLPED	2 2 2
109	Qy 51 NSEFQLYTQDG-ANSFVRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGAC	B 8
50 69	Qy 1 MRWTLVVLCLLEGEGFAFTDWDQYHIVWQDEFDYFDGAKWQHEVTATGGG	B 8
Gaps 17;	Query Match 15.4%; Score 344.5; DB 2; Length 286; st Local Similarity 27.5%; Pred. No. 1.4e-20; atches 112; Conservative 37; Mismatches 96; Indels 163;	ì
0183	A; Residues: 1-266 - SPID A; Cross-references: EMBL:U04836; NID:g450182; PIDN:AAA60459.1; PID:g45018 A; Experimental source: strain 21 C; Genetics: A; Gene: bglA C; Keywords: glycosidase; hydrolase F; 1-30/Domain: signal sequence #status predicted <nat></nat>	##C>C>>>
G.; Palsdottir, A coding for a ther	Accession: \$4201; Accession: \$48201; A	* P P P E 27 C
1999	RESULT 5 \$48201 \$11cheninase (EC 3.2.1.73) precursor - Rhodothermus marinus N;Alternate names: beta-glucanase; endo-beta-1,3-1,4-D-glucanase C;Species: Rhodothermus marinus C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-199	CCCNESE
	361 KWTWDDEGDNNAMQVDYIRVYK 382	.]?
360 669	Dy 303 PEDQNEHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKEFDARGNW : : :	8 성
302 638	OY 249 GLREFYDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLA	B 5
248 608	DY 195 TGGEELGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPN	₽ 6
194 566	135 RTEQKYSFTHGRVVVHAKMÞVGDWLWÞAIWMLÞEDWVYGGWÞRSGEIDIIETIGNRÐFKN 	gg.
134 506	75 PTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARV :	д 6

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C;Keywords: glycoprotein; immune response F;1-17/Domain: signal sequence *status predicted <SIG>F;1-17/Domain: signal sequence *status predicted sprotein *status predicted <MAT>F;18-467/Product: Gram-negative bacteria-binding protein *status predicted F;119,182/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Lee, W.J.; Lee, J.D.; Kravchenko, V.V.; Ulevitch, R.J.; Brey, P.T. Proc. Natl. Acad. Sci. U.S.A. 93, 7888-7893, 1996
A;Title: Purification and molecular cloning of an inducible Gram-neg A;Reference number: JC6150; MUID:96353914
A;Accession: JC6150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gram-negative bacteria-binding protein precursor C;Species: Bombyx mori (silkworm)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997
C;Accession: JC6150; PC6039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
JC6150
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RESULT 7
B72428
Laminarinase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-19
C;Accession: B72428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 42-53; 56-83; 88-100 <LEE2>
A; Experimental source: fat body
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             멁
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A; Residues: 1-467 < LEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comment: This is a soluble protein having affinity for the Gram-negative bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 101;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 GGEFLGIQKMGSTMHWGPGWD-DNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 HGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWP-RSGEIDIIETIGN-----RDFKNT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 14.0%; Score 314; DB 2; Local Similarity 27.3%; Pred. No. 7.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 VWQDEFDYFDGAKWQ-HEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLADNINPQ 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QHMPGFLDDSIYSGTLN---LFSGCTSS-AEACIKQASGADILPPIVSGRI-TSIGFAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAP-FGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDI-PPAMSARVRTFQKYSFT 143
                                                                                                                                                                                                                                                                                        AAGGITEF-RDGSITSGG----VTKPW-----RDSARKASVHFWRHMSDWFPRWSQP---
                                                                                                                                                                                                                                                                                                                                                                                     DGEEWARVEAPRDAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IFEEQFDSLDENVWQIEQYIPIYHPEYPFVSYQRNNLTVSTADGNLHI-----NAKLQ
                                                                                                                                                                                               -SLIVDFVKV 464
                                                                                                                                                                                                                                                                                                                                       AVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRK----FFDARGNWKWTWDDEGDN 370
                                                                                                                                                                                                                                                                                                                                                                                                                               DDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VLYGGPIMDLECRENFLSTKRRRDGTSWGDSFHTYSVQWTPDFIALSV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YGTVEIRAKLPQGDWLYPEILLEPFLKKYGSMNYASGVVKIACARGNAELYSGPNDYSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-467 <LEE1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                             #sequence_revision 11-Jun-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -EAFPAQ------------LVVDYVRVYR 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58; Mismatches 143;
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                                                                                                                                                                                                                                                                                                                                                                                     PAVCAHAPRHLLQAGSQMAPFDDHFYITLGV 408
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                             21-Jul-2000
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A49878

A49878

Coagulation factor G alpha chain precursor - horseshoe crab (Tachypleus tridentatus C;Species: Tachypleus tridentatus C;Date: 30-Jun-1995 #sequence_revision 30-Jun-1995 #text_change 18-Aug-2000 C;Accession: A49878

R;Seki, N; Muta, T; Oda, T; Iwaki, D.; Kuma, K.; Miyata, T.; Iwanaga, S. J. Biol. Chem. 269, 1370-1374, 1994

A;Title: Horseshoe crab (1,3)-beta-D-glucan-sensitive coagulation factor G. A se A;Reference number: A49878; MUID:94117453

A;Accession: A49878

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-673 <SEK>
A;Cross-references: GB:D16622
C;Superfamily: Clostridium xylanase A repeat homology
C;Superfamily: Clostridium xylanase A repeat homology <CXA>
F;437-532/Domain: Clostridium xylanase A repeat homology <CXA>
F;575-670/Domain: Clostridium xylanase A repeat homology <CXA>
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C.M.
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A;Molecule type: DNA
A;Residues: 1-642 <ARN>
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Query Match
Best Local S
Matches 85
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97; Conserv
similarity 21.8%;
85; Conservative
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25.0%;
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Score 209; DB 2;
Pred. No. 3.6e-09;
49; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB:AE000512; NID:g4980496; PIDN:AAD35118.1; PID:g49805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 284; DB 2;
Pred. No. 2.9e-15;
3; Mismatches 102
                                                                                                                                                                                                                                                                                                                                                                                                            457
                                                                                                                                                                                                                                                                                                                            horseshoe crab (Tachypleus tridentatus)
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                             Length 673;
 Indels 150;
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C;Superfamily: Clostridium xylanase A repeat homology
F;361-464/Domain: Clostridium xylanase A repeat homology
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A; Residues: 1-466 <SEE>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Seeger, K.J.; Harris, D.;
submitted to the EMBL Data I
A;Reference number: Z21570
A;Accession: T35164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable secreted glucosidase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #tex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Accession:
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Best Local
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                                                                                                                                                                        GNLRITP-----QRDGAGNWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FFDARGNWKWTWDDEGDNNAMQVDYIRVYK 382
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                                                EIDIME---
                                                                                                                                                                                                                                                                                                 103;
                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL:AL031107;
ce: strain A3(2)
 -FHTFWFDW---
                                                                                                                                                                                                                                                                                                               8.0%;
25.8%;
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                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                               Score 179.5;
Pred. No. 5.6e
28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN:CAA19944.1;
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5.6e-07;
эя
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WDQYHIVWQDEFDYFDG----AKWQHEVTAT--GG----GNSEFQLYTQDGAN-SFVRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QDGANSFYRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGYLDVWAMYGACTNTDNNGCY 118
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                                                                                                                                                                                                                                                                                               GKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPP
                                                                                                                                                                                                                                                                                                                                             WTQ----VFADDFDGAAGSGVNTANWQYDTGTSYPGGPANWGTGEIETMTSSPSNVSLDGG 106
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                                                                                                              EIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWG--PGWDDNRYWLTSLPKHSDDWNYGDN
                                                                                                                                                                                             AMSARVRTFQXYSFTHGRVVVHAKMPV------GDWLWPAIWML--PEDWVYGGWPRSG
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                                                                   ----NT-----GIGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SARLKTQFDKSWKYGKIEAKMAIPSFRGVWVMFWMSGDNTNYVRWPSS
                                                                                                                                                           -ggklrveariqvpnvtgaaakgywpafwmlgapyrgnywnwpgvg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Parkhill, J.; Barrell, B.G.; Library, July 1998
-SPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSPDB:GN00070;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                         -SGRIETKRADFEPP
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RESULT 11
D70525
probable beta-1 - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_ch
C; Accession: D70525
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Church
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentler
Raiandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skel-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Note: A94L
C;Keywords: g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable beta-1,3-glucanase (EC 3.2.1.-) - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 12-Nov-1999
C;Accession: T17584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tatus: preliminary; translated from GB/EMBL/DDBJ .Olecule type: DNA .Residues: 1-364 <GRA> A;Cross-references: EMBL:U42580; NID:g4028896; PIDN A;Experimental source: specific host Chlorella stra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Graves, M.V.; Van Etten, submitted to the EMBL Data A;Reference number: Z18806 F-Accession: T17584
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hes 85; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGTTWNTI----RVEARLKAPRGPGVVGAFWMLPID--NSCFP---EIDIFETPYCERA
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                                                                                                                                                                                                                                                                   NDTDAPYNRPFYIILNTSIGSAWGGIP
                                                                                                                                                                                                                                                                                                                               AVEWNADY IAFYAGDAE - - - - - - TPVFVT - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGA-----AGDIPPAMSA 132
                                                                                                                                                                                                                                                                                 ----APFDQNEHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDAR 357
                                                                                                                                                                                                                                                                                                                                                                                                                        -IG----NRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.6%; Score 148; DB 2; Length 364;
22.2%; Pred. No. 0.00014;
tive 40; Mismatches 108; Indels 1
                          Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D
Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.;
J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares,
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Library, May
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strain NC64A
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                          N.; Holroyd,
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                                                           Gordon,
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Best Local S
Matches 80
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Best Local S
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                           GAPEGTDEMYNGVLDVWAMYGACTNTDNNGCYRTG--AAGDIPPAMSA------
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Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.;
A;Title: Deciphering the biology of Mycobacterium tuberculosis fi
A;Reference number: A70500; MUID:98295987
A;Accession: D70525
A;Status: preliminary; nucleic acid sequence not shown; translati
                                                                                                                                                                                                                             C;Accession: T39920

R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; submitted to the EMBL Data Library, October 1997
A;Reference number: Z21891
A;Accession: T39920
A;Accession: T39920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-294 <COL>
                                                                                                                                                                                                                                                                                                        probable glucanase precursor - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T39920
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                                                                                       C;Genetics:
A;Gene: SPAC21B10.07
A;Map position: 2
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                                                                                                                                           A; Cross-references: EME
A; Experimental source:
                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-419 <MCD>
                                                                                                                                                                                                                Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLFHDEFDGPAGSVPDPSKWQVSNHRTPIKNPVGFDRPQFFGQYRDSRQNVFLDG-----
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56; Conserv
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                                                                                                                                             EMBL:AL121794; PIDN:CAB57923.1; ce: strain 972h-; cosmid c21B10
                                                                                                                                                                                                                                                                                                                                                                                                                                                          294
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               5.9%;
23.1%;
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21.6%;
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H37Rv
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31;
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                 Score 132; DB 2;
Pred. No. 0.0034;
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 81;
                                                                                                                                                                                                                                                                                           Skelton,
                                                                                                                                                                GSPDB:GN00067
                                   Length 419;
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A;Accession: A75132
A;Accession: Preliminary
A;Molecule type: DNA
A;Residues: 1-1144 < KANP
A;Cross references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49770.1; PID:e151566
A;Experimental source: strain Orsay
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WYNDAMRKFFDARGNWKWTWDDEGDNNAM------QVDYIRV
                                                               ----IGGDNGI----
                                                                                                                                                                                                    LDVPYPL-IDAN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLQGANLDKLYIAWDDEYLYIAIKTNNTANWKVAYGIGIDVGPGGFTGSESGDSWGRKIN 125
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                                                                                                            WLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGD
                                                                                                                                                         YWPDYGVAIDVNPGSGIGGTYDPWAKKIYFSGTYLPDYIIYAEAQDGALTWVGLCKW---
                                                                                                                                                                                                                                                   NFIEISLTKVIDGNLDDWNKAELVAQGVPSGIEGANLDRLYVSWDSNYLYIAIKTNNTAK
                                                                                                                                                                                                                                                                                             RYWLTSLPK----HSDDWN------YGDNFHTFWFDWSPNGLRFFVDDENQAL
                                                                                                                                                                                                                                                                                                                                          EKIAIITWI-AGEEGSSAVDTLPVDPSIDYSNINGE------WTDADMLS
                                                                                                                                                                                                                                                                                                                                                                                     E----DWVYGGWPRSGEIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDD----N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---- EFQLYTQDGANSEVRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---NVG-----TSNQVTLHTGDGCEMEDIKRVMTGTALQTNCWVDAPNSYNAGCGVENP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Anthors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subțili A; Accession: B69798
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C; Superfamily: Bacillus subtilis hypothetical protein
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A;Experimental source: strain 168
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C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 05-Dec-1997 #sequence_revision:05-Dec-1997 #text_change 20-Jun-2000
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C;Species: Bacillus subtilis
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97; Conservative
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                                                                                                                                                                            DVPYPLIDANPWWVDFWEWGKPWLPQYENDNP-WAGGTN--LAPFD--QNFHFILNVAVG 317
  ----KWTWDD 366
                                            ----INCLKRLPLRLLSGPTFEYDPATSMLHHMGDGIAGGYHMIIAFGAPQVWMELA
                                                                                                                                                                                                                                NVVHWGCGCKEARISMAGL
                                                                                                                                                                                                                                                                   STMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALL----
                                                                                                                                                                                                                                                                                                                     YDLGGYAWQNNELVPTLWLWQAFFRSGREDIFRMAEAMTRHTSETDSFHLGEYAGLGSRH
                                                                                                                                                                                                                                                                                                                                                               ---GDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIG--NRDFKNTG----GEFLGIQKMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLRYFFEKYPSALEITGLAGSRPKMTIWLWPPDGEAMDLRHYTGNTHVASAYEGFDEMRS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAHGTQNAVWDDVKIV-QDSSDHYSLSKRTGKDYAWVGMLHGSRAKGVCYAGGKNGGVAL 347
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                                                                                       GTNGFIPDGCINR-----GG-----DPALQKPWSNGDWYNDAMRKF--FDARGNW----
                                                                                                                                    DADYALVKTDPMRA-FYEKGKH--PTHARTGPDWAAFCSNWLAEWERTENSEYLKKIETG
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A;Molecule type: DNA
A;Molecule type: CINO
A;Residues: 1-878 <STO>
A;Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB04504.1; GSPDB:GN00
A;Experimental source: strain C-125
C:Genetics:
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Search completed: October 11, 2001, 15:55:28 Job time: 286 sec
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                                                                                                                                                                                          324 --- PDGCINRGGDPALQKPWSNGDW---YNDAMRKFFD 355
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                                                                                                                                                                                                                                                                                                                                                                                                   220 YWLTSLPKHSDDW------NYGDNEHTFWFD--WSPNGLRF--FVDDENQALLDVPY 266
                                                                                                                                     309 QVFPE----GGEPHTSLGIYRPDWAFKSTDTMRDFYD 341
                                                                                                                                                                                                                                               256 RKY-ADSMFLNFW-W---WNHSQERSKQKAASLGRSPYD--LYAGIDVEANGTNTYVNWQ 308
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	yri of of ins: tion tion tisb	ALLS CO INST FU S OF 1,	OF 39- ; Y., Ya beta-1,	.us/Clostridium p; Bacillus.	.ed) sequence update) annotation update) SIDASE A1 PRECURSOR (EC ((1->3)-BETA-GLUCANASE	PRT; 682	ALIGNMENTS	FIBB_HUMAN APE3_YEAST COX1_BRAJA GUB_BACBA ISOA_PSEAY ISOA_PSEAY ISOA_PSESP DESA_SPIPL ACON_GRAVE GUNH_CLOTM GUB_PAEMA GUNG_CLOCE MANA_RHOMR
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·	h a collaboration EMBL outstation - trictions on its is in no way nd for commercial rsib.ch/announce/	GES			> 3) -			homo sapien saccharomyc bradyrhizob bacillus br pseudomonas pseudomonas spirulina p gracilaria clostridium paenibacill clostridium clostridium

Conservative

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Score 351.5; DB 1; pred. No. 1.4e-21; 44; Mismatches 89;

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01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
BETA-GLUCANASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4
(1,3-1,4-BETA-D-GLUCAN 4-GLUCANOHYDROLASE) (LICHENASE).
                          Hydrolase;
SIGNAL
                                                                                                                                                                                                      entities requires a license agreement (some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                           EMBL; U04836;
HSSP; P23904;
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MEDLINE-95010084; PubMed-7925416;
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                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: SHOWS ACTIVITY ON LICHENAN, BETA-GLUCAN AND LAMINARIN BUT NOT ON CMC CELLULOSE OR XYLAN. THE ENZYME HAS A TEMPERATURE OPTIMUM OF 85 DEGREES CELSIUS AND A HOPTIMUM OF 7.0.
CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-BETA-D-GLYCOSIDIC LINKAGES IN BETA-D-GLUCANS CONTAINING 1,3- AND 1,4-BONDS.
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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ACT_SITE
SEQUENCE
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30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update
ENDO-1,3-1,4-BETA-GLYCANASE EXSH (EC 3.2.1.
BLOSTYNTHESIS PROTEIN EXSH):
                      depolymerize nascent succinoglycan chains.";
proc. Natl. Acad. Sci. U.S.A. 95:4912-4917(1998).
-:- FUNCTION: CLEAVES HIGH MOLECULAR WEIGHT SUCCINOGLYCAN TO YIELD I
SUCCINOGLYCAN. DYNAMICALLY REGULATE THE MOLECULAR WEIGHT
DISTRIBUTION OF SUCCINOGLYCAN BY CLEAVING NASCENT SUCCINOGLYCAN
ONLY DURING A LIMITED PERIOD AFTER ITS SYNTHESIS, PERHAPS BEFORE
                                                                                                                                                              "The Rhizobium meliloti exoK gene and prsD/prsE/exsH components of independent degradative pathways which production of low-molecular-weight succinoglycan."; Mol. Microbiol. 25:117-134(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHIME
                                                                                                        CHARACTERIZATION.
MEDLINE-98226741; PubMed-9560202;
York G.M., Walker G.C.;
"The Rhizobium meliloti ExoK and ExsH glycanases
                                                                                                                                                                                                                                                                                                                                                                                                              033680;
30-MAY-2000
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
York G.M., Walker G.C.;
                                                                                                                                                                                                                                                                                                               Rhizobium meliloti (Sinorhizobium meliloti) Plasmid pSymB (megaplasmid 2).
                                                                                                                                                                                                                                                                                       Rhizobiaceae; Sinorhizobium
                                                                                                                                                                                                                                                                                                    Bacteria;
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112; Conserv
 UNDERGOES A TIME-DEPENDENT GREGATION STATE.
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27.5%;
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PROTON DONOR (BY SIMILARITY);
7215C33624135191 CRC64;
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RESULT 4
EGLC_RIME
ID EGLC_R
AC 092302
DT 30-MAY
DT 01-OCT
DE BIOSYN
GN EGLC.
OS Rhizob
OG Plasmi
OC Bacter
OC Rhizob
OX NCBLT
RN [1]
RP SEQUEN
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                                                                                                        30-MAY-2000
30-MAY-2000
01-OCT-2000
ENDO-1,3-1,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exopolysaccharide synthesis; Glycosidase; DOMAIN 275 465 CATALTIC.
ACT_SITE 349 AUCLEOPHILE (
ACT_SITE 354 354 PROTON DONOR SEQUENCE 465 AA; 50286 MW; 6C8482366E9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bidinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                     Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision;
Rhizobiaceae; Sinorhizobium.
  SEQUENCE FROM N.A
                       NCBI_TaxID=382;
                                                                                              BIOSYNTHESIS
                                                                                                                                                                   EGLC_RHIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01034; GLYCOSYL_HYDROL_F16; FALSE_NEG. PROSITE; PS00330; HEMOLYSIN_CALCIUM; FALSE_NEG.
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100 (Rel. 39, Last sequence update)
100 (Rel. 40, Last annotation update)
104 -BETA-GLYCANASE EGLC (EC 3.2.1.-)
11S PROTEIN EGLC).
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PROTON DONOR (BY SIMILARITY);
6C8482366E9E8CA8 CRC64;
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dase; Hydrolase; Plasmid.
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                                             Rhizobiaceae group;
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Prim: PRO0722; Glyco_hydro_16; 1.

Pram: PR00723; hemolysincabind; 1.

PR PRINTS; PR00333; hemolysincabind; 1.

PROSITE; PR00313; CABNDNGRPT.

PROSITE; PS01034; GLYCOSYL_HYDROL_F16; FALSE_NEG.

PROSITE; PS00330; HEMOLYSIN_CALCIUM; FALSE_NEG.
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InterPro; IPR001343; -
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MEDLINE=99413305; PubMed-10485295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: SECRETED. PROBABLY BY A TYPE-III SECRETION SYSTEM (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSEFQLYTQDGANSFYRDGKLFIKPTLLADNINPQTGA-PFGTDFMYNGVLDVWAMYGA- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FANTSADQLHANQFSLALDRSVLTQTFSDDFNTLQLSDGTSGVWDPKYWWAPEKGATLTG
AMRKFFDARGNWKWTWDDEGDNNAMQVDY IRVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDELQWY------VNPT----YQPTASANPFS---VTDGVLTTTAKPASQ
                                                                                                                       YENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYND
                                                                                                                                                                                     TDT----SGFHKYGVLWTEEEIVWYFDDAAIARADTPSDMHD
                                                                                                                                                                                                                                           SDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQ 288
                                                                                                                                                                                                                                                                                                                                                               DWVYGGWPRSGEIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKH
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                                                              MLVNLAIGGMAGPPTDGLM - - GG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 167; DB 1;
; Pred. No. 1.4e-06;
38; Mismatches 113
                                                                                                                                                                                                                                                                                                                                                                                                                             SGMLTTYSSFAQTYGYFEMRADMPDDQGAWPAFWLLPG
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PROTON DONOR (BY SIMILARITY).
; 1BC4A640685E9654 CRC64;
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   381
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There are no restrictions
ong as its content is in
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15-JUL-1999
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DHET_ACEPO
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                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D00635; BAA00528.1;
PIR; S14270; S14270.
HSSP; P22619; 2MTA.
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Kawamura Y., Nishiyama M., Horinouchi S., Beppu T.;
"Cloning and sequencing of the gene cluster encoding two subunits of
membrane-bound alcohol dehydrogenase from Acetobacter polyoxogenes.",
membrane-bound alcohol dehydrogenase from Acetobacter polyoxogenes.",
membrane-bound alcohol dehydrogenase from Acetobacter polyoxogenes.",
membrane-bound alcohol dehydrogenase from Acctobacter polyoxogenes.",
membrane-bound alcohol dehydrogenase from Acctobacter polyoxogenes.",
membrane-bound alcohol dehydrogenase from Acception: METHANOL).
-i- EUNCTION: DEHYDRATION OF PRIMARY ALCOHOL + ACCEPTOR — ALDEHYDE +
-i- CATALYPIC ACTIVITY: PRIMARY ALCOHOL + ACCEPTOR — ALDEHYDE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-NBI1028;
MEDLINE-91159482;
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                                                                                                                                                                                                                                                                                                                      Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                Pfam; PF01011; Bacterial_PQ0; 6.
PROSITE; PS00363; BACTERIAL_PQ0_1; 1.
PROSITE; PS00364; BACTERIAL_PQ0_2; 1.
PROSITE; PS00190; CYTOCHRONE_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                      interPro;
                                                                   212
 259
                                  98
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COPACTOR: PQQ AND HEME.
SUBUNIT: HETEROTETRAMER (DEHYDROGENASE, CYTOCHROME, AND
SWATTER UNKNOWN SUBUNITS) THAT FORMS THE ALCOHOL DEHYDRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE BACTERIAL POO DEHYDROGENASE FAMILY.
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KAYQTWSPTGAWTRQGGGGTVWDSIVYDPVADLVYLGVGNGSPWNYKYRSEGKGDNLFLG 318
                                                                 GNGGSEF-----GARGFVSAFDAETGKVDWRFFTVP--
                                                                                                  GGGNSEFQLYTQDGANSFVR-----
                                GVLDVWAMYGACTNTDNNGC----
                                                                                                                                   78; Conser
                                                                                                                                                                                                                                                                                                                                                                                                    IPR002372;
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                                                                                                                                                                                                                   738 AA;
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(Rel. 23, Last sequence update)
(Rel. 38, Last annotation update)
YDROGENASE [ACCEPTOR] PRECURSOR (E
                                                                                                                                  Conservative
                                                                                                                                                                                                                                   ; PQQ; Heme; 1
35
6 738
6 738
0 650
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                                                                                                                                                                                                                Periplasmic; Membrane; Signal.
POTENTIAL.
POTENTIAL.
ALCOHOL DEHYDROGENASE [ACCEPTOR].
HEME (COVALENT) (BY SIMILARITY).
HEME (COVALENT) (BY SIMILARITY).
IRON (HEME AVIAL LIGAND) (BY SIMILARITY).
MW; 1E2B6ED7BCD92AF6 CRC64;
                                                                                                                                   37;
                                                                                                                                  Score 112.5;
Pred. No. 0.07
Pred. Mismatches
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113;
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                               ---YRTGAAGD----
                                                                 NPKNEPDAASDSVLMN 258
                                                                                                                                                                 Length
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DEHYDROGENASE
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RESULT 6

XYNA_R

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AC P29126

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PIR; S18043; S18043.
PIR; S20907; S20907.
HSSP; P48793; IXND.
InterPro; IPR001000; -.
InterPro; IPR001137; -.
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P29126;
01-DEC-1992 (
01-DEC-1992 (
15-JUL-1999 (
BIFUNCTIONAL
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Zhang J.X., Flint H.J.;
"A bifunctional xylanase encoded by the xynA gene of the rumen
"A bifunctional xylanase encoded by the xynA gene of the rumen
"A bifunctional xylanase encoded by the xynA gene of the rumen
"A bifunctional xylanase encoded by the xynA gene of the rumen
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"A bifunctional xylanase encoded by the xynA gene of the xylanase encoded by the xylanase enc
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    - I - FUNCTION: XYLANASE DOMAIN 1 RELEASES MORE XYLO-OLIGOSACCHARIDES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: IN THE N-TERMINAL SECTION; G (FAMILY 11 OF GLYCOSYL HYDROLASES). SIMILARITY: IN THE C-TERMINAL SECTION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F (FAMILY 10 OF GLYCOSYL HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: XYLAN DEGRADATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND DOMAIN 2 MORE XYLOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APFDQNFHFILN - - - VAVGGTNG
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(Rel. 24, Last sequence update)
(Rel. 38, Last annotation update)
(Rel. 38, Last annotation update)
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PRINTS; PR00134; ĞLHYDRLASE10. PRINTS; PR00911; GLHYDRLASE11. PROSITE; PS00591; GLYCOSYL_HYDROL_F10;

Pfam; PF00331; Glyco_hydro_10; Pfam; PF00457; Glyco_hydro_11;

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Best Local S
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01-AUG-1992 (Rel. 23, La
01-NOV-1997 (Rel. 35, La
BETA-GLUCANASE PRECURSOR
(1,3-1,4-BETA-D-GLUCAN 4
                                                                                                                                                                                                                                                     GUB_BACLI
P27051;
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                   MEDIINE-91224124; PubMed-2026156;
Lloberas J., Perez-Pons J.A., Querol E.;
Lloberas Cloning, expression and nucleotide sequence of the
"Molecular cloning, expression and nucleotide sequence of the
endo-beta-1,3-1,4-D-glucanase gene from Bacillus licheniformis.
Predictive structural analyses of the encoded polypeptide.";
Eur. J. Blochem. 197:337-343(1991).
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                                                                                                                         Bacteria; Firmicutes; Bacillus/Staphylococcus NCBI_TaxID=1402;
                                                                                                                                                               Bacillus licheniformis
                                                                                                 SEQUENCE FROM N.A.
REVISIONS
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77; Conser
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                                                                                                                                                                                     el. 23, Last sequence update)
el. 35, Last annotation update)
PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE)
D-GLUCAN 4-GLUCANOHYDROLASE) (LICHENASE).
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                                                                                                                                                                                                                                                                   STANDARD;
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GLYCOSYL_HYDROL_F11_2;
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19
                                                                                                                                      Bacillus/Clostridium us group; Bacillus.
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ASM/GLM/TRP-RICH (LINKER).
XYLANASE DOMAIN 2.
XYLANASE DOMAIN 2.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
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Pred. No. 0.09
18; Mismatches
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FEBS Lett. 374:221-224 (1995)
-I- CATALYTIC ACTIVITY: HYDROLYSIS OF 1.4-BETA-D-GLYCOSIDIC
-IN BETA-D-GLUCANS CONTAINING 1.3- AND 1.4-BONDS.
-I- MISCELLANEOUS: BETA-GLUCANASES OF BACILIUS HAVE A SUBSTE-
SIMILAR TO LICHENASE OF GERMINATING BARLEY.
-I- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Planas A., Juncosa M., Lloberas J., Querol E.; "Essential catalytic role of Glul34 in endo-beta-1,3-1,4-D-glucan glucanohydrolase from B. licheniformis as determined by site-directions."
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Hahn M., Pons J., Planas A., Querol E., Hein
"Crystal structure of Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  site-directed mutagenesis.";
J. Biol. Chem. 269:14530-14535(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92362869; PubMed-1354172;
Planas A., Juncosa M., Lloberas J.,
"Essential catalytic role of Glul34
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PIR; S15388; S15388.
PDB; 1GBG; 07-DEC-95.
                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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MEDLINE=94237863;
Juncosa M., Pons
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PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
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Tuncosa M., Pons J., Dot T., Querol E., Planas A.;
Tdentification of active site carboxylic residues in Elicheniformis 1,3-1,4-beta--glucan 4-glucanohydrolase
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01-JUN-1994 (Rel. 29, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
STALIDASE PRECURSOR (EC 3.2.1.18) (NET
                                                                                                                                                                                                                                                                                                                                                                                                                         Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P. McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
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                                                                                              CHARACTERIZATION, AND X-RAY CRYSTALLOGRAPHY MEDLINE=92389334; PubMed=1518058; Taylor G.L., Vimr E.R., Garman E.F., Laver F
                                                                                                                                                                           Vimr E.R., Lawrisuk L., Galen J.E., Ka
"Cloning and expression of the Vibrio
nanH in Escherichia coli.";
J. Bacteriol. 170:1495-1504(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-EL TOR N16961 / SEROTYPE 01;
MEDLINE-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C.,
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Wasserman S.S., Kaper J..
"Role of Vibrio cholerae
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MEDLINE-92112298; PubMed-1730470;
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                   226:1287-1290(1992)
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SUBURIT: MONOMER (PROBABLE).
SUBCELLULAR LOCATION: SECRETED.
INDUCTION: MAY BE CONTROLLED BY SEROWTH-PHASE-DEPENDENT MECHANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: CLEAVES THE TERMINAL SIALIC ACID (N-ACETYL NEURAMINIC ACID) FROM CARBOHYDRATE CHAINS IN GLYCOPROTEINS PROVIDING FREE SIALIC ACID WHICH CAN BE USED AS CARBON AND ENERGY SOURCES. SIALIDASES HAVE BEEN SUGGESTED TO BE PATHOGENIC FACTORS IN MICROBIAL INFECTIONS. NANH FACILITATES CHOLERA TOXIN BINDING TO HOST INTESTINAL EPITHELIAL CELLS BY CONVERTING CELL SURFACE POLYSIALGCANGLIOSIDES TO GM1 MONOGANGLIOSIDES. POLYSIALGCANGLIOSIDES TO GM1 MONOGANGLIOSIDES. CAPALYTIC ACTIVITY: HYDROLYSIS OF 2,3-, 2,6- AND 2,8-GLYCOSIDIC LINKAGES JOINING TERMINAL NON-REDUCING N- OR O-ACYLATED RESIDUES TO GALACTOSE, N-ACETYLHEXOSAMINE, OR N- OR O-ACYLATED NEURAMINYL RESIDUES IN OLIOOSACCHARIDES, GLYCOPROTEINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO FAMILY 33 OF SIMILARITY: CONTAINS 4 BNR REPEATS.
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                                                                                                                   VGDWLWPAIWMLPEDWVYGGWP---RSGEIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWG
                                                                                                                                                         MI--VWG--NGSSNTDGVAAYRDIKFEIQGDVIFRGPDRIPSIVASSVTPGVVTAFAEKR 245
                                                                                                                                                                                              GVLDVWAMYGACTNTDNNGCYRT---GAAGDIPPAMSARVRTEQKYSFTHGRVVVHAKMP 154
                                                                                                                                                                                                                                          VLATGTAATEYHKFELVFLPGSNPSASFYFDGK---
                                     PGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLID--
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                                                                                                                                                                                                                                                                                                                                           Similarity
-DTELNLTEQINVSDEFDFSD-
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Pred. No. 0.15;
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(IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no rest
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                                                 EMBL; M80657; AAA34726.1;
EMBL; L33835; AAB59312.1;
PIR; A41624; A41624.
                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                      Roemer T., Paravicini G., Payton M.A., Bussey H.;

"Characterization of the yeast (1-->6)-beta-glucan bios
components, Kreép and Sknlp, and genetic interactions b

PKC1 pathway and extracellular matrix assembly.";

J. Cell Biol. 127:567-579(1994),

J. Cell Biol. 127:567-579(1994),

J. Cell Biol. 127:567-579(1994),

J. CELL BIOL. LOTYMERS OF THE YEAST CELL WALL IN VIVO. IT

FOR FULL ACTIVITY OF BETA-GLUCAN SYNTHASE IN VITRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane protein required for glucan synthesis in v synthase activity in vitro."; Proc. Natl. Acad. Sci. U.S.A. 88:11295-11299(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BETA-GLUCAN SYNTHESIS-ASSOCIATED PROTEIN KRE6 RESISTANCE PROTEIN 6).
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KRE6_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome XVI positions GPH1 and identifies two novel tRNA genes."; yeast 10:1527-1530(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-95176711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roemer T., Bussey H.;
Yeast beta-glucan synthesis: KRE6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92107936;
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                        Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
MEDLINE-95014745;
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15-JUL-1998
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SUBCELLULAR LOCATION:
SUBCOMPARTIMENT.
                                                                                                                                                                                                             SIMILARITY: STRONG,
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                                     S0006363; KRE6.
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                                                                                                                                                                                                                                                    TYPE
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                       Cell wall; Signal-anchor
CYTOPLASMIC
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AN SYNTHASE OR
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Matches 82
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CARBOHYD
"Two beta-glycanase genes are clustered in Bacillus polymyxa: molecular cloning, expression, and sequence analysis of genes encoding a xylanase and an endo-beta-(1,3)-(1,4)-glucanase.";
J. Bacteriol. 173:7705-7710(1991).
-I- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-BETA-D-GLYCOSIDIC LIIN BETA-D-GLUCANS CONTAINING 1,3- AND 1,4-BONDS.
                                                                                                                                                                                                              GUB_PAEPO STANDARD; PRT; 238 AA.

P45797;

01-NOV-1995 (Rel. 32, Created)

15-JUL-1996 (Rel. 32, Last sequence update)

15-JUL-1998 (Rel. 36, Last annotation update)

BETA-GLUCANASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE)
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CARBOHYD
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                                                                                                    SEQUENCE FROM N.A. STRAIN=ATCC 842;
                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Staphylococcus
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                                                                                       MEDLINE=92041687; PubMed=1938968;
                                                                                                                                     NCBI_TaxID=1406
                                                                                                                                                                             Paenibacillus
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micutes; Bacillus/Clostridium gr
hylococcus group; Paenibacillus.
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19.0%;
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N-LINKED (GLCNAC. . .) (PO
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N-LINKED
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(POTENTIAL).
(POTENTIAL).
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              LINKAGES
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Best Local
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Q44002; 007952;
15-DEC-1998 (Rel
15-DEC-1998 (Rel
15-JUL-1999 (Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X57094; CAA40379.1; -. HSSP; P23904; 1CPM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ÷
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases | CATALYTIC ACTIVITY: PRIMARY ALCOHOL + ACCEPTOR = ALI REDUCED ACCEPTOR. | COFACTOR: PQQ AND HEME (BY SIMILARITY).
                                                                                                    Bacteria; Proteobacteria;
Gluconacetobacter.
MCBI_TaxID=33995;
                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DTL-1999 (Rel. 38, Last annotation update)
ALCOHOL DEHYDROGENASE [ACCEPTOR] PRECURSOR (EC 1.1.99.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; pF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement
                                                    STRAIN-DES11 / Thurner C.A.K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
                                                                                                                                            Acetobacter europaeus
                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro; IPR000757; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANGE SIMILAR TO LICHENASE OF GERMINATING BARLEY.
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                            THGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFLGI
                                                                                                                                                                                                                                                                                                       KHTATTNIP----STPGKIMMNLWNGTGVDSWLGSYNGANP
                                                                                                                                                                                                                                                                                                                               ENQALLDVPYPLIDANPWWVDFWEWG----KPWLPQYENDNP
                                                                                                                                                                                                                                                                                                                                                                                 QKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYG----DNFHTFWFDWSPNGLRFFVDD--
                                                                                                                                                                                                                                                                                                                                                                                                            SHG----
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                                                                                                                                                                                                                                                                                                                                                         -KDTTKVQF-----NYYTNGVGGHEKIINLGFDASTSFHTYAFDWQPGYIKWYVDGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKYSF-
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238 /
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                                                                                                                                alpha subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 106;
Pred. No. 0.
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BY SIMILARITY.
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NUCLEOPHILE (BY SIMILARITY).
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                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COCF7B4EA5D40E8C CRC64;
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ID OSTA_HAEIN
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DT 01-NOV-1995
DT 01-NOV-1995
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Best Local :
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BINDING
METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01011; Bacterial_PQQ; 6.
PROSITE; PS00363; BACTERIAL_PQQ_1;
PROSITE; PS00364; BACTERIAL_PQQ_2;
PROSITE; PS00190; CYTOCHROME_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X82894; CAA58066.1;
EMBL; Y09480; CAA70688.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HETEROTETRAMER (DEHYDROGENASE, CYTOCHROME, AND TWO SMALLER UNKNOWN SUBUNITS) THAT FORMS THE ALCOHOL DEHYDROGEN COMPLEX (BY SIMILARITY).
SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING THE PERIPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPACE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNGGSEF-----GARGFVTAFDAETGKVDWRFFTAP
                                                                                                                                                             ONFHFILN - - - VAVGGTNG
                                                                                                                                                                                          AKQAFVKDLK---
                                                                                                                                                                                                                      GLRFFYDDENQALLDVPYPLIDANPWWVDFWE----WGKPWLPQYENDNPWAGGTNLAPFD
                                                                                                                                                                                                                                                  NFAAMAFSP----KTGLYYIPAQQVPFLYTNQVGGFTPHPDSWNLGLDMNKVGIPDSPE
                                                                                                                                                                                                                                                                                --STMHWGPGWDDNRYWLTSLP-----
                                                                                                                                                                                                                                                                                                                                                                 LGSIVALKPETGEYVWHFQETPMDQWDFTSVQQIMTLDLPINGETRHVIVHAPKNGFFYI
                                                                                                                                                                                                                                                                                                                                                                                              -----IPPAMSARVRTFQ-----KYSFTHGRVVVHAKMPVGDWLWPAIWMLP-----
                                                                                                                                                                                                                                                                                                                                                                                                                            NKAYQTWSPTGAWTRQGGGGTVWDSIVYDPVADL-VYLGVGNGSPWNYKYRSEGKGDNLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----QTGAPFGT-----
                                                                                                                                                                                                                                                                                                           IDAKTGEFISGKNYVYVNWASGLDPKTG-----RPIYNPDALYTLTGKEWYGIPGDLGGH
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IPR001479;
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651
655
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                                                            STANDARD;
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651
654
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80944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Periplasmic; Membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -DFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGD---
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HEME (COVALENT) (BY SIMILARITY).
IRON (HEME AXIAL LICAND) (BY SIM
E681BB237ACB91F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
ALCOHOL DEHYDROGENASE [ACCEPTOR].
                                                            PRT;
                                                                                                                                                                                          -GWIVAWDPQKQAEAW--RVDHKGPWNGGILATGGD
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                                                            782 AA
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                                                                                                                                                                                                                                                                              --KHSDDWNYGDNFHTFWFDWSPN
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Best Local S
Matches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   influenzae Rd.";
Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=RD / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANIC SOLVENT TOLERANCE IMP OR OSTA OR HI0730.
Haemophilus influenzae.
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                          336
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                                                                                                                                         224
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                                                                                                                                                                                                                                                                                                                                          106 FDYKD------GKADNIT--
                                                                                                                                                                                                                              192
385 LDFNYHKYDLANGWLNFKLHSQAVR--FD
                                                                                                                                                                                                                                                                                                               86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                          --HGRVVVHA----
                                                                                                             -- KRHLFYWNHNSSFLQNW
                                                                                                                                        SLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWE-WG
                                                                                                                                                                      TFTPKYMSRRGWQANGEFRYLTSIGE--
                                                                                                                                                                                                ---PEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLT
                                                                                                                                                                                                                           MWHARFKIHGVPVFYTPYLQLPIGDRRRSGLLIPSAGTSSQDGLWYAQPIYWNIAPNYDL
                                                                                                                                                                                                                                                                                                              TGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSA-RVRTFQKYSFT-
                                                                                                                                                                                                                                                                                                                                                                     FDYFDGAKWQHEVTATGGGNSEFQLYTQDG--ANS---FV-RDGKLFIKPTLLADNINPQ 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U32756; AAC22389.1;
HI0730; -.
                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an email to license@isb-sib.ch).
                                                                                --- WLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGF-IPDGCINRGGDPA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        782
                                                                                                                                                                                                                                                                                                                                                                                                 4.7%;
llarity 21.3%;
Conservative
                                                                                                                                                                                                                                                                                  -LHNN-----YRVMKNATFTSCLH----GDNAWAVDASEIRQYVKEEYAE
                          -LQKPWSNGDWYNDAMRKFFD
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A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90084 MW;
                                                                                                                                                                                                                                                         ---KMPVG---
                                                      ARIAYYQPNYNFSLS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OUTER MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                b; Score 106; DB
b; Pred. No. 0.26
46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Small K.V., Fraser C.M., Smith H o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gamma
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ORGANIC SOLVENT TOLERANCE
HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E73C8A5786B02D1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subdivision; Pasteurellaceae;
                                                                                                                                                                      -GKVAGEYLG
411
                          355
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                                                                                                             RLNINYTRVSDKRYFNDFDSIYG
                                                                                                                                                                                                                                                                                                                                                                                                  112;
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                                                      AHQFQIFDDIVNIGPYRAVPQ
                                                                                                                                                                                                                                                         DWLW---PAIWML-----
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 782;
                                                                                                                                                                      KVRYSEYASDNR----
                                                                                                                                                                                                                                                                                                                                                                                                  Indels 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a collaboration - MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                         282
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InterPro; IPRO0757; -.
InterPro; IPRO01137; -.
Pfam; PF02018; CBD_6; 1.
Pfam; PF02018; CBD_6; 1.
Pfam; PF00727; Glyco_hydro_1; 1
PRINTS; PR00737; GLHYDRIASE16.
PRINTS; PR00911; GLHYDRIASE11.
PROSSTE; PS00776; GLYCOSYL_HYDROI
             ACT_SITE
ACT_SITE
ACT_SITE
DOMAIN
DOMAIN
DOMAIN
                                                                                                                CHAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                   EMBL; S61204;
HSSP; P23904;
                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
XYLANASE/BETA-GLUCANASE PRECURSOR (INCLUDES: ENDO-1,4-BETA-XYLANASE
(EC 3.2.1.8) (XYLANASE); (ENDO-BETA-1,3-1,4 GLUCANASE) (EC 3.2.1.73)
(1,3-1,4-BETA-D-GLUCAN 4-GLUCANOHYDROLASE) (LICHENASE)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q53317;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 175:2943-2951(1993).
-I- FUNCTION: CONTAINS TWO CATALYTIC I.
-BETA-1,3-1,4 GLUCANASE ACTIVITIES
-I- CATALYTIC ACTIVITY: ENDOHYDROLYSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glucanase domains, flavefaciens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flint H.J., Martin J., McPherson C. "A bifunctional enzyme, with separa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                         PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruminococcus flavefaciens
                                                                                         DOMAIN
                                                                                                      DOMAIN
                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93259938; PubMed-8491715;
                                                                                                                                                                  Multifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LINKAGES IN XYLANS.

CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-BETA-D-GLYCOSIDIC LINKAGES
IN BETA-D-GLUCANS CONTAINING 1,3- AND 1,4-BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G (FAMILY 11 OF GLYCOSYL HYDROLASES). SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: XYLAN DEGRADATION. SIMILARITY: IN THE N-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLYCOSYL HYDROLASES.
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                                                                                                                                                                                                                                                                                                                       1AJK.
                                                                                                                                                                                                                                                                                                                                 AAB26620.1;
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                                                                                                                                                                    enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35, Created)
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                 ydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with separate xylanase ded by the xynD gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENDOHYDROLYSIS
   ž
                                                               LINKER.
C (BETA-GLUCANASE).
NUCLEOPHILE (BY SIMILARITY)
PROTON DONOR (BY SIMILARITY)
                           NUCLEOPHILE (BY POLY-THR. POLY-THR.
                                                                                                                                        XYLANASE/BETA-GLUCANASE
                                                                                                                                                       POTENTIAL.
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                                                                                                                                                                               Glycosidase;
                                                                                                                            (XYLANASE)
   2880A689647284AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECTION;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Daniel A.S., Zhang J.-X.; xylanase and beta(1,3-1,4)-gene of Ruminococcus
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                                                                 (BY SIMILARITY).
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                                                    SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                         restrictions
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RESULT 14
GUB_BACAM
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 Query Match
Best Local
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P07980;
P07980;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
BETA-GLUCANASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE)
(1,3-1,4-BETA-D-GLUCAN 4-GLUCANOHYDROLASE) (LICHENASE).
             Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                    Hofemeister J., Kurtz A., Borriss R., Knowles J.;
"The beta-glucanase gene from Bacillus amyLoliquefaciens shows
extensive homology with that of Bacillus subtilis.";
Gene 49:177-187(1986).
-i- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-BETA-D-GLYCOSIDIC LINKAGES
-i- RETA-D-GLUCANS CONTAINING 1,3- AND 1,4-BONDS.
-i- MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANGI
SIMILAR TO LICHENASE OF GERMINATING BARLEY.
                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus/Staphylococcus
NCBI_TaxID=1390;
                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                            PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
                                                                          Pfam; PF00722; Glyco_hydro_16;
                                                                                                                                          EMBL; M15674; AAA87323.1;
                                                                                                                                                                         or send
                                                                                                                                                                                          entities requires a license agreement
                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87192007; PubMed=3106158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BE 20/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus amyloliquefaciens.
                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             763
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                                                                                                                           A29091; A29091.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----WVDFWEWGKPWLPQY------ENDNPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKHEKLYDLGFDSSEAYHTYGFDWQPNYIAWYVDGREVYRATQDIPKTPGKIMMNAWPGL
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                                                                                                                                                                         an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                           IPR000757;
                             Glycosidase; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -WYKRNAVINDGCLQLSIDQKWTNDKNPD-----WDPRYSGGEFRTNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 105;
Pred. No. 0.
BETA-GLUCANASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPRSGEIDIIETIGNRDFKNTGGEF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   group
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SEQUENCE
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P87023;
01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                            entities
or send a
                                                                                                                                                                                                                                           "Isolation of the Candida albicans homologs of Saccharomyces cerevisiae KRE6 and SKN1: expression and physiological function.";
J. Bacteriol. 179:2363-2372(1997).
-:- FUNCTION: INVOLVED IN THE SYNTHESIS OF (1->6)- AND (1->3)-BETA-D-GLUCAN POLYMERS OF THE YEAST CELL WALL IN VIVO. IT IS REQUIRED FOR FULL ACTIVITY OF BETA-GLUCAN SYNTHASE IN VITRO. IT MAY BE A BETA-GLUCAN SYNTHASE, PART OF A MULTIPROTEIN GLUCAN SYNTHASE OR
                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                         Glycoprotein;
DOMAIN
                                                                                                        modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRE6
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                                                   EMBL; D88490; BAA19593.1;
                                                                                                                                                                                                                                                                                                                                           Yamada-Okabe H.;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-97234650;
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                                                                                                                                                                                        SUBCOMPARTIMENT.
SIMILARITY: STRONG,
                                                                                                                                                                                                                    SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. GOLGI
                                                                                                                                                                                                                                 A MODULATOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYEVRMKPAKNTGIVSSFFTYTGPTE--GTPWDEIDIEFLGKDTTKVQFNYYTNGAGNHE
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                                                                            s requires a license agreement (See http://www.isb-sib
an email to license@isb-sib.ch).
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                                                                                                    non-profit institutions as long as its content and this statement is not removed. Usage by an
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239
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(Rel. 35, Last seq
(Rel. 35, Last ann
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                                      Transmembrane;
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abe T., Yabe T.,
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         Cell wall; Signal-anchor.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II ME
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BY SIMILARITY.
; A76A64268A7AAAOB CRC64;
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Saccharomycetales;
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CARBOHYD
657 -LILNLGISNNWAYIDWPSISEPVTFRIDYVRVYQ 690
                                                        627 --GDDP-----TLTVYSQALH----- 656
                                                                                                                         594 VTWYEFGDNAHNF----QTYGYEYLNDPETGYL-----
                                                                                                                                                   229 SDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQ 288
                                                                                                                                                                                   534 SSGKKENCGVASQSLQLAPMDIWYIPDYNWVEIYNFSVSTMNTYTGGPFQQALSATTMLN 593
                                                                                                                                                                                                                                                  474 YSYDSCDAGITPNQSSPDGISYLPGQRLNKCTCPGELHPNRGVGRGAPEIDVIEGEVMTD 533
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                                                                                       289 YENDNEWAGGTNLAPFDONFHFILNVAVGGTNGFIPDGCINRGGDPALOKPWSNGDWYND 348
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Search completed: October 11, 2001, 15:57:06 Job time: 298 sec

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Result
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Perfect score:
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  1 MRWTLVVLCLLFGEGFAFTD......DDEGDNNAMQVDYIRVYKRN 384
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Q9u0g4 pacifastacu
Q2660 strongyloce
017492 anopheles g
Q9n189 bombyx mori
Q45095 bacillus ci
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Q9vsr4
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Q9nhb0
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         1 oerskovia x
8 manduca sex
0 drosophila
3 bombyx mori
3 oerskovia x
3 hyphantria
4 drosophila
8 drosophila
8 thermotoga
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9 bombyx mori
5 bacillus ci
5 drosophila
8 clostridium
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4.8	4.8	4.8	4.8	4.8	4.9	4.9	5.0	5.1	5.2	5.4	5.6	5.6	5.9	6.2	6.6	8.0	8.2	8.5	9.3	10.7	11.1	11.1	11.5	12.3	12.7
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Q9p6t0 neurospora	084907 zobellia ga	Q06472 saccharomyc	013789 schizosacch	080803 arabidopsis	074170 aspergillus	Q9rii9 aeromonas s	Q9m0d2 arabidopsis	P93670 hordeum vul	Q9ker4 bacillus ha	060019 phaffia rho	O31530 bacillus su	Q9v0d4 pyrococcus	Q9usw3 schizosacch	007242 mycobacteri	Q84415 paramecium	088021 streptomyce	Q9kwf3 clostridium	Q91816 streptomyce	Q27082 tachypleus	Q9ewr5 streptomyce	Q9nha9 drosophila		073951 pyrococcus	Q9f3a0 streptomyce	Q9wxn1 thermotoga

ALIGNMENTS

8	Qy	Db	Qy	뫄	Qy	W B O	ŞQ	DR	RL	RT	ŖΤ	RT	RA	RΑ	RX	RΡ	R	õ	8	3 6	2 2	DE	ָרָדָי בין]]	DŢ	AC	Ħ	077072	RESULT	
121 GAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGE 180	121 GAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGE 180	61 GANSEVRDGKLFIKPTLLADNINPQTGAPEGTDEMYNGVLDVWAMYGACTNTDNNGCYRT 120	61 GANSEVRDGKLFIKFTLLADNINPQTGAPEGTDEMYNGVLDVWAMYGACTNTDNNGCYRT 120	1 MRWTLVVLCLLFGEGFAFTDWDQYHIVWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQD 60	1 MRWTLYVLCLLFGEGFAFTDWDQYHIVWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQD 60	Query Match 100.0%; Score 2240; DB 5; Length 384; Best Local Similarity 100.0%; Pred. No. 1e-182; Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps	SEQUENCE 384 AA; 44322 MW; C90B5C94003BAD6D CRC64;	٠	J. Biol. Chem. 273:24948-24954(1998).	activation of prophenoloxidase cascade.";	binding protein from Eisenia foetida earthworm involved in the	"Identification and cloning of a glucan- and lipopolysaccharide-	., Gomez J., De Baetselier P., '		9840615	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=6396;	Lumbricina; Lumbricidae; Eisenia.	Elikarvota: Metazoa: Annelida: Clitellata: Oligochaeta: Haplotaxida:	CCEI.	COELOMIC CYTOLYTIC FACTOR 1.	01-NOV-1998 (TEMBLIEL 08, LAST annotation update)	(TrEMBLrel. 08,	(TrEMBLrel. 08,	077072;	O77072 PRELIMINARY; PRT; 384 AA.	72.	LT 1	

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Matches 148
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01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Lee S., Wang R., Soderhall K.;
"A lipopolysaccharide and beta-1,3-glucan-binding phemocytes of the freshwater crayfish Pacifastacus Lepurification, characterization, and cDNA cloning.";
J. Biol. Chem. 275:1337-1343(2000).
EMBL: AJ250128; CAB65353.1; -.
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Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
Astacoidea; Astacidae; Pacifastacus.
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01-MAY-2000 (TEEMBLrel. 13, Last sequence update)
01-MAY-2000 (TEEMBLrel. 13, Last annotation update)
LIPOPOLYSACCHARIDE AND BETA-1,3-GLUCAN BINDING PROT
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                                          PYPLIDANPWWVDFWEWGKFWLPQYENDNPWAGGTNLAPFDQNFHFILNVAYGGTNGFIP
                                                                                           MGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDV
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 DGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWD-DEG---DNNAMQVDYIRV
                                                                               AGSTLHWGPNPQANMFLKTHKTYSANDGSFANNFHIWRMDWTRDNMKFYVDDQLQLTVDP
                                                                                                                                                                                    TSKWYSEHFLFNDELN----LGDKCTDHRDYGCVRKGTSEHIINPIMSAKFTTHPSFAFRY
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SEQUENCE FROM N.A.

K MEDLINE-96270625; PubMed-8692900;

K MEDLINE-96270625; PubMed-8692900;

R Bachman E.S., McClay D.R.;

T "Molecular cloning of the first metazoan beta-1,3 glivery of the sea urchin Strongylocentrotus purpuratus.";

T of the sea urchin Strongylocentrotus purpuratus.";

T proc. Natl. Acad. Sci. U.S.A. 93:6808-6813(1996).

RRL Proc. Natl. Acad. Sci. U.S.A. 93:6808-6813(1996).

DR EMBL; U49711; AAC47235.1; -.

DR EMBL; U49711; AAC47235.1; -.
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PUTATIVE GRAM N
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; S
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                                                                                                                                                                          01-OCT-2000 (Tremblrel. 15, 01-OCT-2000 (Tremblrel. 15, 01-OCT-2000 (Tremblrel. 15, BETA-1,3-GLUCAN RECOGNITION
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Molecular immune responses of the mosquito Anophel
bacteria and malaria parasites ";
Proc. Natl. Acad. Sci. U.S.A. 94:11508-11513(1997).
                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Pterygota; Neoptera; Endopterygota; Lepidog Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                            Bombyx mori (Silk moth).
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       NCBI_TaxID=7091;
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Nematocera; Culi
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Last annotation update)
PROTEIN PRECURSOR.
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Pred. No. 5.
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                                                                      oda; Insecta;
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045095, Q53369;
01-NOV-1996 (TIEMBLIEL 01
01-NOV-1996 (TIEMBLIEL 01
01-MAR-2001 (TIEMBLIEL 11
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MEDLINE=94033858; PubMed=7764221; Yanamoto M., Aono R., Horikoshi K.; Yanamoto M., Aono R., Horikoshi K.; PubMed=1841165 and properties of the enzyme accumulated Escherichia coli carrying the gene."; Biotechnol. Biotechnol. Biotechnol. 57:1518-1525(1993). EMBL; D17519; BAA04469.1; -.
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SEQUENCE
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SIGNAL
                                                                                                                   Bacillus circulans.
Bacteria; Firmicutes; Ba
Bacillus/Staphylococcus
NCBI_TaxID=1397;
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SEQUENCE
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EMBL; AB026441;
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                                                                                      SEQUENCE FROM N.A. STRAIN-IAM1165;
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hem. 275:4995-5002(2000).
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X SHOWA;
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PubMed=10671539;
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Pred. No. 3e-2
i7; Mismatches
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BETA-1,3-GLUCAN RECOGNITION
; 09249039F7456BF2 CRC64;
                                                                                                                                                                                                                                                                                                                                 - ISNKPWKNS - - ATKAMLKFWDARSQWFPTWDED - -
                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390.5;
No. 3e
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                                                                                                                                                                                                update)
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                                             Bacillus circulans the periplasm of
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                                            periplasm
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m the
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                                                                                                                                                                                                                                                                                                                                 482
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                                                                                                                                                                                                                                                                                                                                                                                                                    394
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                                                                                                                                                                                                                                                                                                                                                                                                                                       256
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RESULT
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Best Local Sin
Matches 103;
                                                                                                                                                                                                                                                                                                                   Q9VVR5;
Q9VVR5;
01-MAY-2000
01-MAY-2000
01-MAR-2001
MEDITINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
George R.A., Cavis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
SIGNAL
                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01034; GI SMART; SM00409; IG;
                                                                                                                                                                                                                                                                                         GNBP1 OR CG6895.
                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=BERKELEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rro; IPR000757; -.
rro; IPR003343; -.
rro; IPR003599; -.
rro; IPR00358; -.
rpe02368; Big_2; 1.
ITE; PS01034; GLYCOSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDEGDNNAMQVDYIRVYK 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDENQALLDVPYPLIDANPWWVDFWEWGK------PWLPQYENDNPWAGGTNLAPFDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFV
:|:| | | | : :::|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TMQVDYVRVYK 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFYLIMNLAIGGTFDGGRTPD----PSDIPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SG------AVHFGGQWPTNRY-LSGEYHFPEGQTFANDYHVYSVVWEEDNIKWYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -ALNEPKSFPQDPSRY-----AQYS----AQYS----SGKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLIWQDEFNGTALDQSKWNYETGYYLNDDPNTWGWGNSELQHYTDRAQNVFVQDGKLNIK 486
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39
877 ·
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O (TrEMBLrel.
1 (TrEMBLrel.
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877
95451
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27.2%;
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Last sequence up
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Pred. No. 3.
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C4D2CFF93019446C
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                                                                                                                                                                                                                                                                                                                                                                            492
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3.7e-23;
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                                                                                                                                                                                                                                             Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    645
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RESULT
Q59328
ID Q5
AC Q5
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DT 01
DT 01
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RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., McShrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Peinert K., Remington K., Saunders R.D.C., Scheeler F., Smith T.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Syliskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Yiliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,

RA Yell, Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Yeng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,

RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT The genome sequence of Drosophila melanogaster.";

RESOLUTIONE S. SALL M. S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
Q59328;
Q59328;
01-NOV-1996
01-NOV-1996
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandry Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Duurbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harris
Hostin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KYSFTHGRVVVHAKMPVGDWLWPAIWMLP-EDWVYGGWPRSGEIDIIETIGNRDFKNTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTGAPFGTDFMYNGVLDVWAMYGACTNTDN--NGCY----RTGAAGDIPPAMSARVRTFQ 138
                                                                                                                                                                                                                            -ALKIDYVRVF
                                                                                                                                                                                                                                                                       NAMOVDYIRVY
                                                                                                                                                                                                                                                                                                                       SLGVSVGGFGDF----
                                                                                                                                                                                                                                                                                                                                                                       ILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDN
                                                                                                                                                                                                                                                                                                                                                                                                                          LFSVDGQVYGEMLNGFTELDENP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLVD----GRSLYGGP------VLSTDAHQREDLWLSKRKISHFGDDFHTYSLDWSSNRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLFEETFDQLNESLWIHDVRLPLDSKDAEFVLY--DG-KAKVHDGNLVIEP-LLWSSYRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101;
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                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                       381
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27.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 357; DB 5; Pred. No. 2.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C5D0E5E61FABB779 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                     1324
                                                                                                     ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133;
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Lai Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chandra
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                                                                                                                                                                                                                                                                                                                                                                                                                        430
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(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

01, 01,

Created)
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Best Local Similarity 27.2%;
Matches 100; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schwarz W.H., Schimming S., Fuchs K.P., Staudenbauer W.L.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-1- CATALYTIC ACTIVITY: EMDOHYDROLYSIS OF 1,3- OR 1,4-LINKAGES IN
BETA-D-GLUCANS WHEN THE GLUCOSE RESIDUE WHOSE REDUCING GROUP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Clostridium.
                                                                             01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-DSM 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium thermocellum.
                    Rhodothermus marinus
Bacteria; CFB group;
NCBI_TaxID=29549;
                                                                                                                 052754;
                                                                                                                            052754
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SEQUENCE FROM N.A.
                                                                     LAMINARINASE.
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                                                                                                                                                                                                                                                       GGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVD
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                                                                                                                                                                                                                                                                                                                                                                       KSWKYGKFEIRAKMPQGQGIWPAIWMMPEDEPFYGTWPKCGEIDIMELLGHEP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycosidase.
                                                                                                                            PRELIMINARY;
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                                 Rhodothermus
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                                                                             Last sequence update)
Last annotation updat
                                                                                                     Created)
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Pred. No. 1.6e-21;
1; Mismatches 93
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                                 group;
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                                 Rhodothermus
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Best Local S
Matches 116
                                                                                                                                                                                                                                                                                   068641;
                                             Parrado J., Escuredo P.R., Coneje
Asenjo J.A., Dobson C.M.;
"Molecular characterisation of a
                                                                                                                      Ventom
Enzyme
[2]
                                                                                                                                                                                   Oerskovia xanthineolytica.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Micrococcineae; Cellulomonadaceae; Cel
NCBI_TaxID=1826;
                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ITI278;
BORTISS R., Krah M.;
Submitted (PEB-1998) to the EMBL/GenBank/DDBJ database:
EMBL; AF047003; AAC69707.1; -.
InterPro; IPR000757; -.
Pfam; PF00722; Glyco_hydro_16; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; I.
SEQUENCE 276 AA; 32028 MW; 6D303D5FB04B48DE CRC64;
                                                                                   SEQUENCE FROM N.A.
STRAIN=LL G109;
MEDLINE=96409238; PubMed=8814220;
  STRAIN-LL G109;
            SEQUENCE FROM N.A.
                                  Biochim.
                                            Derskovia xanthineolytica.
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                                                                                                                                                                                                                                                                                                                                                                                                        VYGG--WPRSGEIDIIETIG-NRD-----FKNTGGEFLGIQKMGSTMHWGPGWDDNRYW
                                                                                                                                                                                                                                                                                                                                                                       LQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIRVYK
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                                                                                                                               A.M., As
Microb.
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                                Biophys.
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                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                Asenjo J.A.;
b. Technol. 13:71-75(1991).
                                                                                                                                                                                                                                                                                                                                                    -----EAFPAQ------LVVDYVRVYR
                                  Acta
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                                                                            Conejero-Lara F.,
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Last sequence update)
Last annotation update)
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                                                       thermoactive
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                                                                            Kotik M.,
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                                                       beta-1,3-glucanase from
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                                                                                                                                                                                                Cellulomonas.
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                                                                          Ponting
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                                                                            C.P.,
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RESULT Q9NJ98
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AC Q9
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Best Local S
Matches 103
                                                                                                                                                                                                                                                                                                                        Q9NJ98 PRELIMINARY; cn., Q9NJ98; Q9NJ9
                                                                                                                                                                                                                     Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Di
Sphingiodea; Sphingidae; Sphinginae; Manduca.
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Pfam; PF00652; Ricin_B_lectin; 1.
Pfam; PF00722; Glyco_hydro_16; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
SMART; SM00458; RICIN; 1.
SEQUENCE FROM N.A.
TISSUE-FAT BODY;
MEDLINE-20179841; PubMed-10713054;
Ma C., Kanost M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-96250169; PubMed-8659924; Ferrer P., Hedegnard L., Halkier T., Diers I., Savva D., Asenjo J Ferrer P. Hedegnard L., Halkier T., Jers I., Savva D., Asenjo J Molecular cloning of a lytic beta-1,3-glucanase gene from Oerskc xanthineolytica LLG109. A beta-1,3-glucanase able to selectively permeabilize the yeast cell wall."; permeabilize the yeast cell wall."; Acad. Sci. 782:555-566(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ferrer P., Andrews B.A., Asenjo J.A., Hedegaard L., Diers Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AF052745; AAC38290.1; -.
HSSP; P23904; lAJK.
                                                                                                                                                                                         NCBI_TaxID-7130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-LL G109;
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Pred. No. 7.1e-22;
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se gene from Oerskovia
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01-OCT-2000 (Tremblrel. 15, Last sequence update)
01-MAR-2001 (Tremblrel. 16, Last annotation update)
GRAM-NEGATIVE BACTERIA BINDING PROTEIN 1.
GNBPL OR CG6895.
                                                                                                                                           "Molecular cloning and functional analysis of Gram-negative bacteria binding protein family. Submitted (JAN-2000) to the EMBL/GenBank/DDBJ EMBL; AF228472; AAF33849.1; -.
                                                                                                                                                                                                                                                                                                                                                                                          Q9NHBO;
                                                                                                                        FlyBase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agglutinates Microorganisms and Activates J. Biol. Chem. 275:7505-7514 (2000). EMBL; AF177982; AAF44011.; - SEQUENCE 487 AA; 54567 MW; 3BA4869C5AL
                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                         SEQUENCE FROM N.A.
Kim Y.S., Ryu J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A betal,3-Glucan Recognition Protein from an Insect, Manduca sexta, Agglutinates Microorganisms and Activates the Phenoloxidase Cascade.
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LLFEETFDQLNESLWIHDVRLPLDSKDAEFVLY--DG-KAKVHDGNLVIEPLLWSS----
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                                                     Score 323; DE
Pred. No. 1.6e
5; Mismatches
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Pred. No. 4.5e-20;
5; Mismatches 135;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
GRAM-NEGATIVE-BINDING PROTEIN PRECURSOR (GNBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE TISSUE-FAT BODY, AND HEMOLYMPH; MEDLINE-96353914; PubMed-8755572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bombyx mori (Silk moth).

Eukaryota; Metazoa; Arthropoda; Tracheata;

Pterygota; Neoptera; Endopterygota; Lepidop

Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                 Signal; Glycoprotein; SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-7091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Purification and molecular cloning of an inducible gram-negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CUTICULAR EPIDERMAL CELLS.
DEVELOPMENTAL STAGE: EXPRESSION
OR MICROBIAL CHALLENGE.
                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO H.CUNEA GRAM-NEGATIVE-BINDING PROTEIN. SIMILARITY: WEAK, TO FAMILY 16 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                 INDUCTION: BY BACTERIAL INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDNNAMQVDYIRVY 381
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                                           VWQDEFDYFDGAKWQ-HEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLADNINPQ 85
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L38591; AAB40946.1; -.
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IFEEQFDSLDENVWQIEQYIPIYHPEYPFVSYQRNNLTVSTADGNLHI--
                                                                                          101;
                                                                                        Similarity 27.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
780652FC89046E77 CRC64;
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Q1-WQV-1996 (TrEMBL)
Q1-WAY-2000 (TrEMBL)
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BETA-1,3-GLUCANASE
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PROSITE;
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   GIQKMGSTMHWGPGWD-DNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQ
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: | | | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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                                                                   QPQFGRIEARIQIPRGQGIWSAFWMVGANLPDTPWPTSGEIDIMENVGNAPHEVHG----
                                                                                                                                      SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL
                                                                                                                                                                                                                                                                                                                                             LAWSDEFDGAAGSAPNPDVWNHETGAGGWGNAELQNYTTSRVNSAL-DGQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWP-RSGEIDIIETIGN----RDFKNT
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                                                                                                                                                                                                                                                                      NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00722; Glyco_hydro_16; 1.
TE; PS01034; GLYCOSYL_HYDROL_F16;
NCE 306 AA; 32835 MW; CD8DB8C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Similarity
95; Conser
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Firmicutes; Actinobacteria; Actinobacteridae;
etales; Micrococcineae; Cellulomonadaceae; Cel
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AAC44371.1; -.
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Last sequence update)
Last annotation updat
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Pred. No. 2.1e-18;
6; Mismatches 97;
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Best Local Similarity
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Insect Biochem, Mol. Biol. 28:827-837(1998).
-I- FUNCTION: MAY BE INVOLVED IN THE INSECT-IMMUNE PROTEIN. IT PRESENT STRONG AFFINITY TO THE CELL WALLOF GRAM-NEGATIVE BACTERIA.
-I- SUBCELLULAR LOCATION: SECRETED.
-I- DEVELOPMENTAL STAGE: EXPRESSION STARTS A FEW MINUTES AFTER AN INUTRY OR MICROBIAL CHALLENGE THEN STAYS RELATIVELY HIGH FOR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE-99035790; PubMed-9818384;

Shin S.W., Park S.-S., Park D.-S., Kim M.G., Kim S.C., Brey P.T.,

Park H.-Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TERMBLIEL. 10, Created)
01-MAY-1999 (TERMBLIEL. 10, Last sequence update)
01-MAY-2000 (TERMBLIEL. 13, Last annotation.update)
GRAM-NEGATIVE-BINDING PROTEIN (FRAGMENT).
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-1- SIMILARITY: WEAK, TO FAMILY 16 OF GLYCOSYL HYDROLASES EMBL; AF023916; AAD09290.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Di
Noctuoldea; Arctiidae; Hyphantria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNBP1.
                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Insect immunity.
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                                                                                                                                                                                                                                                                                                                                                                                                                  OR 24 HOURS.
INDUCTION: BY BACTERIAL INFECTION
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KNT---GGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNG 249
                                                                                                       --QQRMPGFTDSSIYSGSLNI---FSGCT-APAEACMKDAWGASILPPVVSGRI-TSKAF 261
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                                                                                                                                      NPQTGAPFGTD-FMYNGVLDVWAMYGACTNTDNNGCYRTG-AAGDIPPAMSARVRTFQKY 140
                                                                                                                                                                     IFEENFNTFREDVWQIEQYIPVYSTEFPFVSYQHLSQDPTVA-VTGGNLRITPKL----
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481 AA;
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53014 MW;
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                                                                                                                                                                                                                                            Score 302; DB 5; Pred. No. 9.7e-18;
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                                                                                                                                                                                                                                Mismatches 146;
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                                                                                                                                                           250
                                                                                                                                                                                         322 SNKMLFGGPVMNLQ-CYDTLLESKASSNGRQW------GDDFHEYVLRWAPER 367
P----QLLVDYVKV 478
                              EGDNNAMQVDYIRV
                                                                                           NFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDD 366
                                                                                                                                                           LRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNP---WAGGTNLAPFDQ 306
                                                             HFYLTLGVAAGSITEF-PDGVQTSGSRP---KPWTNTG--SKAMLHFWEDMDSWFATWNQ 468
                                                                                                                             ITLSVDGVEWARVEPTASGLSGR-
                              380
                                                                                                                             -FPQTCSKLPRTFLAAGTKMAPFDD
                                                                                                                             414
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